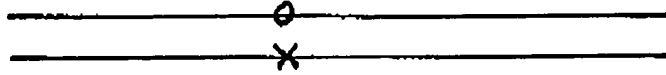
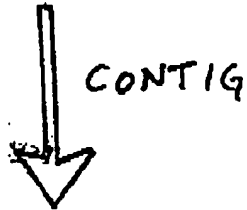


____ PUBLIC
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o REF
 X SNP (VARIANT)



KNOWN
 NOVEL

FIG. 1

20250216

TABLE 1

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cg43333349	1008	CGCTGACAGGGG AGTCTGAGCCACA [A/G]ACCCGCTCA CCCGAGTGCACG CACG	A	G	Gln	Gln	SILENT- CODING	ATPase_as sociated	Human Gene SWISSPROT- ID:P20648 POTASSIUM- TRANSPORTING ATPASE ALPHA CHAIN (EC 3.6.1.36) (PROTON PUMP) (GASTRIC H+/K+ ATPASE ALPHA SUBUNIT) - HOMO SAPIENS (HUMAN), 1035 aa.	0	19
2	cg43931765	2296	ATGGATAGTCCAT CTGGTTGGATGC A/TGTGTACTCGT TGGCCTCGTTCAG GT	A	T	Thr	Thr	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3

3	cg44130533	1832	AATACAAAGCTGA GTGGAGAGCAGT T/GJGGTGAAGAAG TATGGCATTCCAA GT	T	G	Val	Val	SILENT- CODING	cadherin	Human Gene SWISSNEW- ID:P13591 NEURAL CELL ADHESION MOLECULE, 140 KD ISOFORM PRECURSOR (N-CAM 140) (NCAM-140) (CD56 ANTIGEN) - HOMO SAPIENS (HUMAN), 848 aa.lpcis:SWISSPROT-ID:P13591 NEURAL CELL ADHESION MOLECULE, 140 KD ISOFORM PRECURSOR (N-CAM 140) (NCAM- 140) (CD56 ANTIGEN) - HOMO SAPIENS (HUMAN), 848 aa.	0	11
4	cg34888922	2330	TATTGTTATTATGT ATTCTGTTTACIA/ GJTGTTTCTGTGTC ACTGCTAAGAGAA	A	G	Thr	Thr	SILENT- CODING	cadherin	Human Gene SWISSNEW- ID:Q08554 DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3) - HOMO SAPIENS (HUMAN), 894 aa.lpcis:SWISSPROT-ID:Q08554 DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3) - HOMO SAPIENS (HUMAN), 894 aa.	0	18

5	cg34888922	815	CAAGGAGCATTGA CCGTGAGAAATA CTTGAACAGTTTG CGTTATATGGCTA TG	C	T	Tyr	Tyr	SILENT- CODING	cadherin	Human Gene SWISSNEW- ID:Q08554 DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2/DG3) - HOMO SAPIENS (HUMAN), 894 aa. Jcsl:SWISSPROT-ID:Q08554 DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3) - HOMO SAPIENS (HUMAN), 894 aa.	0	18
6	cg40310734	1172	TGGCGTCGTATTT TGGGCATTCAGT G/C/GCTGTCACCTG ACGTCAACGGGG ATG	G	C	Val	Val	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
7	cg40310734	2243	AGGGGGCCTATG AAGCAGAGCTGG C/C/GGTGACACCT GCCCCAGGGCGC CCACT	C	G	Ala	Ala	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
8	cg40310734	812	GTTACTGTGAAGC GGGCTTCAGCTC C/GGTGGTCACTC AGGCCGGAGAGC TGG	C	G	Ser	Ser	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)

9	cg43331935	1922	GTGACAAGTACTT CATAGAGGATGGI GTTGGCCTGGTCA TCCACAGCCTGG ACT	G	T	Gly	Gly	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P32004 NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1) - HOMO SAPIENS (HUMAN), 1257 aa.	0	X
10	cg42388009	383	AAGGAGAAAACAA TGAAGAACCGAA CTTGAAGACGAAG ACTCTGAGGCTGA GA	C	T	Asn	Asn	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL- BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
11	cg42388009	389	AAAACAATGAAGA ACCGAACGGAAG CTTGAAGACTCTG AGGCTGAGAATAC CA	C	T	Asp	Asp	SILENT- CODING	cadherin	Human Gene SWISSPROT- ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL- BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
12	cg44126574	1289	AGAACGGCCAGC CCCTGTGGATCCT [C/G]GGGGATGTC TTCCTCAGGTCCT ACT	C	G	Leu	Leu	SILENT- CODING	cathepsin	Human Gene SPTREMBL- ID:Q64411 PROGASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSIN C) - CAVIA PORCELLUS (GUINEA PIG), 394 aa.	8.00E-155	6 (6p21.3)

13	cg43970983	3066	GGACTCCAGTGT CCAGGGCATCCA GIC/TTACATCCTA TCCTGGCGGCCA CTCA	C	T	Ser	Ser	SILENT- CODING	collagen	Human Gene SWISSPROT- ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG- CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
14	cg44032748	245	TAAGACGGGCAG CTACACCCGCAG C/A/G]GTTACCTG CCAGCTGAGCAA CTGGT	A	G	Ala	Ala	SILENT- CODING	complement	Human Gene SWISSPROT- ID:P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 584 aa.	0	1 (1p32)
15	cg41553795	222	TCCAGCCCCAAGG CCAAATTTTGATGCI T/G]CAGCAGTTTG CAGGGACCTGGC TCC	T	G	Ala	Ala	SILENT- CODING	complement	Human Gene Homologous to SWISSPROT-ID:P07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa.	1.40E-104	9 (9q34.3)
16	cg43942011	1371	AGGTAGGAGGGC TTGGTCTCCAAAC [A/G]CCTATTGTTT CATTCTCCACAGT GC	A	G	Gly	Gly	SILENT- CODING	complement recept	Human Gene Similar to TREMBLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
17	cg21644442	1219	AACAGCCGGCAG ATGTAAGTGGTAC [A/C]GCCTTGCCC AGGGTGGGCCCC GTGA	A	C	Thr	Thr	SILENT- CODING	csf	Human Gene SWISSPROT- ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)

18	cg41533258	597	TCCAGGCCCGGG CAGGAGGGGTCC T[G/A]GTTGCCTC CCATCTGCAGAG CTTCC	G	A	Leu	Leu	SILENT- CODING	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPROETIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107	17 (17q11.2)
19	cg43996714	1743	ATGTGCCCCACTGC ATTGGGTTGTCC A/GGGAGTTGATA CTGGTGGGATCA CAG	A	G	Pro	Pro	SILENT- CODING	dehydrogenase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11
20	cg43259523	366	CAGAAATATGGAG GCACAGGAGCTT C/A/T/T/T/T/T/TATCC ACTGTGCTCGTGA TAG	A	T	Ser	Ser	SILENT- CODING	dehydrogenase	Human Gene SWISSPROT- ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2.00E-229	25

21	cg43057018	1528	GAATAAGAAATTC AATCTGGATGCA C/TGTGGTACCCA TACCCTGCCTTT GA	C	T	Leu	Leu	SILENT- CODING	dehydrogen- ase	Human Gene SWISSNEW- ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa. Jpcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
22	cg1395871	430	GTGCTCCAGAGG GGCCAGCAGGCA C[A/G]GGAAAAAC CGAAACACACCAA GGACT	A	G	Thr	Thr	SILENT- CODING	dynein	Human Gene Homologous to SPTREMBL-ID:Q92816 CYTOPLASMIC DYNEIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	
23	cg1395871	436	CAGAGGGGCCAG CAGGCACAGGAA A[A/G]ACCGAAAC CACCAAGGACTTG GCTA	A	G	Lys	Lys	SILENT- CODING	dynein	Human Gene Homologous to SPTREMBL-ID:Q92816 CYTOPLASMIC DYNEIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	
24	cg1395871	542	AGCAATGGGAAA GTTTTTAAAGGA C/TGTGCTTCTTC TGGTGCTTGGGC TTG	C	T	Leu	Leu	SILENT- CODING	dynein	Human Gene Homologous to SPTREMBL-ID:Q92816 CYTOPLASMIC DYNEIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	

25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

25	cg1395871	571	CTTCTTCTGGTGC TTGGGCTTGCTT C/TTGATGAATTCA ACCGGATTGAGTT GG	C	T	Phe	Phe	SILENT- CODING	dynein	Human Gene Homologous to SPTREMBL-ID:Q92816 CYTOPLASMIC DYNEIN 3 HEAVY CHAIN - HOMO SAPIENS (HUMAN), 197 aa (fragment).	2.50E-103	
26	cg43950268	1269	AGCGGCCCAACCA TGGCCCTAGGGT CIG/ATCAACAAGT CCAGCAGCAATCA TGG	G	A	Asp	Asp	SILENT- CODING	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
27	cg43918531	461	CCGATGGCTATGA GCAGGCTGCTCG C/TGTGCTATTG AACACCTGGACAA GA	C	T	Arg	Arg	SILENT- CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.lpcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

CG43957743 1146 CAAAGTTCCTCAAT C

28	cg43957743	1146	CAAAGTTCCTCAAT AAAGTGGCAGTTT C/TTTCAGGTTCTA CTGGCTCCACTTC TC	T	Glu	Glu	SILENT- CODING	esterase	Human Gene SWISSNEW- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). lpcis:SWISSPROT- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.90E-178	
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29	cg43319420	963	TCACCCCTCAGGA GGTGGCTGTTCT G[C/T]GTCCACGA CAACTACAGAAAC AACC	T	Cys	Cys	SILENT- CODING	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcls: SWISSPROT-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
30	cg3001932	1631	TCTTCAACATCGT CTATTGGCTTTA[C /T]TATGTGAAC TA AAACATGGCCTCC C	T	Tyr	Tyr	SILENT- CODING	gaba	Human Gene SWISSPROT- ID:P47870 GAMMA- AMINO BUTYRIC-ACID RECEPTOR BETA-2 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 474 aa.	1.90E-256	334
31	cg43975899	370	GGATTTTGGACAG ACTCCTAGATGG[C/T]TATGACAATC GCCTGAGACCAG GAT	T	Gly	Gly	SILENT- CODING	gaba	Human Gene SWISSPROT- ID:P14867 GAMMA- AMINO BUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 456 aa.	1.30E-248	5 (5q34)

32	cg43299024	1643	GGGCCCACCTTCC CCCTGGACGTCC A[A/G]TGGAAACGA CCTGGACTACATG GACT	A	G	Gln	SILENT- CODING	glucoamylase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
33	cg43299024	2021	TGAACGAGCCCTTC CAACTTCATCAG[G/A]GGCTCTGAG GACGGCTGCCCC AACA	G	A	Arg	SILENT- CODING	glucoamylase	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
34	cg43969076	443	AATCCAAATGAG CTCTCCAACACACI G/A]TATTTCTGC GTTTTGATCCAG AC	G	A	Tyr	SILENT- CODING	glucuronidase	Human Gene SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA- G1) - HOMO SAPIENS (HUMAN), 651 aa.	0	7 (7q21.11)
35	cg43969014	325	AATCCAGATGAG CTCTCCAACACACI G/A]TATTTCTGC GTTTTGATCCAG AC	G	A	Tyr	SILENT- CODING	glucuronidase	Human Gene Similar to SWISSPROT-ID:P08236 BETA- GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.40E-80	5
36	cg43065549	880	GGACCATCTCTGT GACCACACCTGCI G/A]GACGCTGTCA TTGGCCCACTACTC GC	G	A	Ala	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

37	cg43065549	991	ACCCCTGGAATAGT AGAGGATGCTGT T/GJTTCCTGAAGA ATGAGGCTCAGC GCA	T	G	Val	Val	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID: P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
38	cg44004239	1141	TGACGTCATCCAT GTCCAATGTCCA C/TACCATGGCCC CCCCAAAATGCTC TC	C	T	Val	Val	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID: Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN- DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
39	cg44004239	1846	GAAGGGATATAAC TGAAGCAATAAA C/TJTTCACGGT TGGCAAATGTGGA CA	C	T	Lys	Lys	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID: Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN- DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
40	cg43957605	1677	AGGACTGTTTTTC ATTCAGCTTCAG/A /CJGTGATCCCAT GGGCTCTTCTGTG A	A	C	Thr	Thr	SILENT- CODING	glycoprotein	Human Gene SWISSPROT- ID: Q00013 55 KD ERYTHROCYTE MEMBRANE PROTEIN (P55) - HOMO SAPIENS (HUMAN), 466 aa.	3.10E-249	X (Xq28)

41	cg40915005	1229	ATGTCTCAGGATT CTACCCAAAGCC C/TGTGTGGTGA TGTGGATGCGGG GTG	C	T	Pro	SILENT- CODING	glycoprotein	Human Gene SWISSNEW- ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T- CELL SURFACE ANTIGEN T6/LEU- 6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.lcls:SWISSPROT-ID:P06126 T- CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)
42	cg40356255	1210	TGGCAATAATAGT GCCTTCCCTTGCT C/TCTTTTGCTAT GCCTTGCATTATG GT	C	T	Leu	SILENT- CODING	glycoprotein	Human Gene SWISSNEW- ID:P29016 T-CELL SURFACE GLYCOPROTEIN CD1B PRECURSOR (CD1B ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.lcls:SWISSPROT-ID:P29016 T- CELL SURFACE GLYCOPROTEIN CD1B PRECURSOR (CD1B ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.	6.70E-183	1 (1q21)

43	cg44004667	1183	CTGTGATATCTAC ATCTGGCGCCCI C/TJTGCCCGGA CTTGCGGGTCCT TCT	C	T	Leu	Leu	SILENT- CODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P01732 T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T- LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.jpcls:SWISSPROT-ID:P01732 T- CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR (T-LYMPHOCYTE DIFFERENTIATION ANTIGEN T8/LEU-2) - HOMO SAPIENS (HUMAN), 235 aa.	7.60E-127	
44	cg43068999	544	AGGGTCTGCGAC AGGGTTACTTTGTI G/AJGAAGCTCAGC CCAAGATTGTCCT GG	G	A	Val	Val	SILENT- CODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P02743 SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA- 1-GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 223 aa.	1.60E-119	1 (1q21)
45	cg41568631	1242	ATGGCCAGTGCT GGGTCTTTGCTG G/C/AJGTGACCAC CACAGTGCTGCG CTGCC	C	A	Gly	Gly	SILENT- CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)


46	cg41568631	1545	GCTCTGTGGAGT CCATCAAGAAATGG [C/G]CTGGTCTAC ATGAAGTACGACA CGC	C	G	Gly	Gly	SILENT- CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
47	cg41603916	361	GCATCCAGTGGG TAGGGGACCCCTC G[C/T]TGGAAGGA TGGCTCCATTGTC ATAC	C	T	Arg	Arg	SILENT- CODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q91406 IP1=CNS MYELIN P0- LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
48	cg41603916	409	TACACAACCTAGA CTACAGTGACAA[T/C]GGCACGTTCA CTTGTGACGTCAA AA	T	C	Asn	Asn	SILENT- CODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q91406 IP1=CNS MYELIN P0- LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
49	cg34317662	465	AGTCCCTTCTCCG TGGCACCTACGC[G/C]TATGGTTTG AGAAGCCCTCTG CCA	G	C	Ala	Ala	SILENT- CODING	helicase	Human Gene Homologous to SWISSPROT-ID:Q12099 PROBABLE ATP-DEPENDENT RNA HELICASE FAL1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 399 aa.	3.60E-120	17
50	cg43983917	1353	AGTCCTTACTTTGC CATTAAACCACAA[C /T]CCCGACGCCAA GGACTTGAAGCA GC	C	T	Asn	Asn	SILENT- CODING	homeobox	Human Gene SWISSPROT- ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	

51	cg43983917	1359	ACTTTGCCATTAA CCACAACCCCGA[C/T]GCCAAGGACT TGAAGCAGCTCG CGC	C	T	Asp	Asp	SILENT- CODING	homeobox	Human Gene SWISSPROT- ID:P50458 HOMEOBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.30E-216	
52	cg42730678	979	TGGAGCGAGCGT GGATCCAGTTCCG C/G/T]GCGGGGT GTTTGGGTCAAGT TGCT	G	T	Ala	Ala	SILENT- CODING	homeobox	Human Gene SWISSPROT- ID:P28356 HOMEOBOX PROTEIN HOX-D9 (HOX-4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2
53	cg42714160	689	GTTACCAGACGCT GGAGCTGGAGAA[G/A]GAGTTTCACT ACAATCGCTACCT GA	G	A	Lys	Lys	SILENT- CODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEOBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
54	cg43959084	810	TCAGGTAGCGATT GTAGTGAAATTCIT /C]TTCTCCAGCTC CAGGGTCTGGTA GC	T	C	Lys	Lys	SILENT- CODING	homeobox	Human Gene Homologous to SWISSPROT-ID:P09629 HOMEOBOX PROTEIN HOX-B7 (HOX-2C) (HHO.C1) - HOMO SAPIENS (HUMAN), 217 aa.	1.30E-113	
55	cg42359655	1124	GGAAGCATTG CCAATCAGTCCAG [A/G]GCGGAAAGG GATGCCTTCCTGC AGG	A	G	Arg	Arg	SILENT- CODING	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLCERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)

56	cg42359655	2468	ACAGCCAGCGGT TTGGCCTGCACCA [C/T]GTCAACTTCA GCGACAGCAGCA AGT	C	T	His	His	SILENT- CODING	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLKERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)
57	cg42359655	4340	ATCTGGTCACCCCT GCAGAACCTGGG] C/T]GTGTCCCACT ACCGTTTTTCCAT CT	C	T	Gly	Gly	SILENT- CODING	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLKERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)
58	cg43998672	1329	TGGTGTGGGCCT TGGTGAACCTCTAG [C/A]ACGCGGCTA ATGCTCTCCTGGTT TGG	C	A	Val	Val	SILENT- CODING	hydroxyster oid	Human Gene SPTREMBL- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
59	cg43922672	1689	GGAAGCTGACTC CAGAGGCCATGC C[C/T]GACCTCAA CTCCTCCACTGAC TCTG	C	T	Pro	Pro	SILENT- CODING	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15

60	cg42908571	630	GTAGTGAGGAAC AAGCCAGAGCTG TIG/CJCAGATGAG TACAAAAGTCCTG ATCC	G	C	Val	Val	SILENT- CODING	interleukin	Human Gene Homologous to SWISSPROT-ID: P05231 INTERLEUKIN-6 PRECURSOR (IL- 6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
61	cg43942050	181	AGTTGGAAGTGAA TGGATCGCAGCAI C/TTCACITGACCT GTGCTTTTGAGGA CC	C	T	His	His	SILENT- CODING	interleukinre cept	Human Gene SWISSNEW- ID: P16871 INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA) (CDW127) (CD127 ANTIGEN) - HOMO SAPIENS (HUMAN), 459 aa. IpcIs: SWISSPROT-ID: P16871 INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL- 7R-ALPHA) (CDW127) (CD127 ANTIGEN) - HOMO SAPIENS (HUMAN), 459 aa.	3.10E-249	5 (5p13)

62	cg43145505	1249	TAAATATTCGAGA CATTGACAAGAT C/TJTATGTTTCGAA CAGGTATCTACCA TG	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSNEW- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa. pcds:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0	3
63	cg43918241	1693	AGATCTTTGAGGA AGGGGAATCTGA C/TJGATGAGTTTG ACATGGATGAGAA TC	C	T	Asp	Asp	SILENT- CODING	kinase	Human Gene SPTREMBL- ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0	3
64	cg43090990	1438	TTCTGACGCACAT GTTTTGTACATTTC /TTCAGACCAAGGA AAACCTCTTTTT G	C	T	Phe	Phe	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC- THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0	10

65	cg43969763	2339	TTAGTATCATTCA CTGTGATCTAAAJA /GJCCTGAAAATAT CCTTCTTTGTAAC C	A	G	Lys	Lys	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:Q13627 SERINE/THREONINE- SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0	21 (21q22.1)
66	cg42879455	2062	AGGTATATACCAT CATGTACAGTTGTT /CJTGGCATGAGAA AGCAGATGAGCG TC	T	C	Cys	Cys	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0	X (Xq21.3) 
67	cg42659872	1744	TGGCTCCGGCTA CACCACATCATG [A/C]GGGTGCTAA GCATATCCTGAGA CGC	A	C	Arg	Arg	SILENT- CODING	kinase	Human Gene SPTREMBL- ID:Q16715 PYRUVATE KINASE (EC 2.7.1.40) - HOMO SAPIENS (HUMAN), 587 aa (fragment).	9.80E-308	1 (1q21)

68	cg42506800	1323	GCTTGCCCAATTTC TCGTCTGTATGCI A/CJAAGTACTTTTC AAGGAGATCTGAA TC	A	C	Ala	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:Q16654 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 4) - HOMO SAPIENS (HUMAN), 411 aa.lpcis:SPTREMBL- ID:Q16654 PYRUVATE DEHYDROGENASE KINASE ISOFORM 4 - HOMO SAPIENS (HUMAN), 411 aa.	1.60E-220	7 (7q21.3)
69	cg43966621	526	CTGTGGAGTACAT GTAGCTGAAGAGI C/TJCGCTCAATCT TCCTCAAGGGAAC AC	C	T	Arg	Arg	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.lpcis:SPTREMBL- ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.80E-219	17
70	cg43917871	1448	ACATCATATTGGC GCTGCTGACGGGI C/TJGTACTGCCCC CTGGCATGCTAGA TG	C	T	Thr	Thr	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)

71	cg43917871	1526	CAGGTAGAAATA GGGTGCTCCAT T/GGCCCTCTCTG CAGTAAGCCGTG ACT	T	G	Ala	Ala	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
72	cg44131752	912	AGCTCAATGGTG GCTCTGCGTGCT C/G/AJTCCCGAAG TGACCTGCCTGGT TCCG	G	A	Ser	Ser	SILENT- CODING	kinase	Human Gene SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	16
73	cg43969473	1765	AATCAACCCACT CATCTATGGCAAJT /CJGATGTGGATTC TGTGGATGTTGCA A	T	C	Asn	Asn	SILENT- CODING	kinase	Human Gene SPTREMBL- ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.10E-154	
74	cg44025829	610	AGACCCCGCCGT CCCCTGGCCAAG CTT/CJGTGGAGTG CTGCCAAGGGGA CTGGT	T	C	Ala	Ala	SILENT- CODING	kinaserecep tor	Human Gene SWISSPROT- ID:Q04771 ACTIVIN RECEPTOR TYPE I PRECURSOR (EC 2.7.1.-) (ACTR-I) (SERINE/THREONINE- PROTEIN KINASE RECEPTOR R1) (SKR1) (ACTIVIN RECEPTOR-LIKE KINASE 2) (ALK-2) (TGF-B SUPERFAMILY RECEPTOR TYPE I) (TSR-I) - HOMO SAPIENS (HUMAN), 509 aa.	7.90E-283	2

75	cg43318277	1107	CTCACGCTTTGCA GTCATCTGGTCC G/AJCCTAGCACTC CCTCCTCTCCTCG GC	G	A	Pro	Pro	SILENT- CODING	MHC	Human Gene SPTREMBL- ID:Q02646 MHC BINDING PROTEIN 2 - HOMO SAPIENS (HUMAN), 2500 aa.	1.20E-247	6
76	cg43966144	632	TTAACACGAGGGA GCCTGTGATGCT G/AJGCTGCTATG TGTGGGGCTTCTA TC	G	A	Leu	Leu	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147	6 (6p21.3)
77	cg42686658	644	CCCCTGTGATCAA TATCACCTGGCT A/GJCGCAACGGC CAAACCTGTCACTG AGG	A	G	Leu	Leu	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
78	cg42686658	857	CACCACCAGATG CCATGGAGACCC T[G/A]GTCTGTGC CCTGGGCCTGGC CATCG	G	A	Leu	Leu	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
79	cg42686658	869	CCATGGAGACCC TGGTCTGTGCCCT [G/A]GGCCTGGCC ATCGGCCTGGTG GGCT	G	A	Leu	Leu	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)

Genetic Information for the HLA Class II Region

80	cg42686658	881	TGGTCTGTGCCCT GGCCCTGGCCAT C/TJGGCCTGGTG GGCTTCCTCGTG GGCA	C	T	Ile	Ile	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
81	cg42686658	893	TGGGCCCTGGCCA TCGGCCTGGTGG G/C/GITTCCTCGT GGCACCGTCCT CATCA	C	G	Gly	Gly	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
82	cg42686658	905	TCGGCCTGGTGG GCTTCCTCGTGG G/C/TJACCGTCCT CATCATCATGGGC ACAT	C	T	Gly	Gly	SILENT- CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
83	cg38337333	279	GTTTCCTCATTAG CCCTGTGACCCCI A/TJGCACACGCAG GGACCTACAGAT GTC	A	T	Pro	Pro	SILENT- CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
84	cg38337333	492	TTGACATCTACCA TCTATCCAGGGA G/AJGGGGAAGCC CATGAACCTAGGC TCC	G	A	Glu	Glu	SILENT- CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19

85	cg38337333	699	CTTCTAGTAGTTG GCCTTCAACCCACI T/AJGAACCAAGCT TCAAAACTGGTAT CG	T	A	Thr	Thr	SILENT- CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
86	cg38337333	774	GGTACTCAGTGG CCATCATCCTCTT C/TACCATCCTTC CCTTCTTTCTCCT TC	C	T	Phe	Phe	SILENT- CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
87	cg38337333	783	TGGCCATCATCCT CTTCACCATCCTT /CJCCCTTCTTTCT CCTTCATCGCTGG T	T	C	Leu	Leu	SILENT- CODING	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	
88	cg43984759	649	AGGAGCTCAAGC GTGAGGCCGAGA C/C/TCTACGGGA GCGGGAAGGCGA GGAGT	C	T	Thr	Thr	SILENT- CODING	misc_chann el	Human Gene SPTREMBL- ID:Q14193 H-DRK1 K(+) CHANNEL - HOMO SAPIENS (HUMAN), 858 aa.	0	20
89	cg39660131	990	TCATGGGCAACCT AAGGCACAAAGTG C/TJGTGCGCAACT TCACAGCGCTCAA CG	C	T	Cys	Cys	SILENT- CODING	misc_chann el	Human Gene SPTREMBL- ID:Q14524 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 2016 aa.	0	3 (3p24)

90	cg44963814	717	CGGAATACCTGG CCATCACCTCTGA [A/G]AGCAAAGAG AACTGCACGGGC GTCC	A	G	Glu	Glu	SILENT- CODING	misc_chann el	Human Gene Homologous to SWISSPROT-ID:Q07699 SODIUM CHANNEL BETA-1 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 218 aa. pcis: TREMBLNEW-ID:G2804300 VOLTAGE-GATED SODIUM CHANNEL BETA-1 SUBUNIT - HOMO SAPIENS (HUMAN), 218 aa.	2.20E-113	19 (19q13.1)
91	cg21413267	870	AGAGTGCGGAGT GGGTCAATCGTGG A/C/T]GCCCGTGGG CACCTACAACACC AGGA	C	T	Asp	Asp	SILENT- CODING	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	7.90E-79	
92	cg21413267	909	ACAACACCCAGGAA GTACGAGTGCTG[C/T]GCCGAGATCT ACCCGGGACATCA CCT	C	T	Cys	Cys	SILENT- CODING	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	7.90E-79	
93	cg3000465	1160	AGAGGCTCTTTCT GCAGAAACTTCC[A/C]AAATTACTTT GCATGAAAGATCA TG	A	C	Pro	Pro	SILENT- CODING	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	6.10E-70	8 (8p11.2)

94	cg30421838	3766	GTCTAGGATGGA GATCCTACAACA C/TTGTCAGTGGG CAGATGCTGTATT TTG	C	T	His	His	SILENT- CODING	nucl_recpt	Human Gene SWISSNEW- ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.lpcds:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
95	cg30421838	4114	ATAACTTGCATGA TCCTTGTCAAACA /GCTTCATCTGTA CTGCTTGAATACA T	A	G	Gln	Gln	SILENT- CODING	nucl_recpt	Human Gene SWISSNEW- ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.lpcds:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
96	cg43947341	713	TTACGTCGCCAA TTCCCAGGGCACI A/GTTGCCGACGA ACTTCAGTACGGG AT	A	G	Asn	Asn	SILENT- CODING	nuclease	Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa.	1.10E-115	
97	cg43939230	4226	TCCCTGTGACCCA GGCAGGTGCATG A/GGTGACACTGG TCGTGACCTGGC CAG	A	G	Thr	Thr	SILENT- CODING	oncogene	Human Gene SPTREMBL- ID:Q99907 LATENT TRANSFORMING GROWTH FACTOR-BETA-BINDING PROTEIN- 2 - HOMO SAPIENS (HUMAN), 1821 aa.	0	14 (14q24)

98	cg42674136	1447	CGGCACACAGGC CGCTCGCCGGAG C/C/TGTGGCCCA CCCCAGCCCCCT GGCCA	C	T	Ala	Ala	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:P31314 HOMEBOX PROTEIN HOX-11 (TCL-3 PROTO- ONCOGENE) - HOMO SAPIENS (HUMAN), 330 aa.	3.70E-182	10
99	cg41972699	742	AGAACTCGCGGG TCTCCCACTACAT C/TATCAACTCGC TGCCCAACCGCC GTT	C	T	Ile	Ile	SILENT- CODING	oncogene	Human Gene Similar to SWISSPROT-ID:Q64010 PROTO- ONCOGENE C-CRK (P38) (ADAPTER MOLECULE CRK) - MUS MUSCULUS (MOUSE), 304 aa.	2.40E-84	22 (22q11)
100	cg42849556	963	CTGCAACTACCTT GAACCAAGTTGAG C/TTCGGGATCCA CCCTCAGCAGCA GCC	C	T	Leu	Leu	SILENT- CODING	oxidase	Human Gene SWISSPROT- ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67- PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.80E-287	25
101	cg43996195	1310	CAGCATGACCTG GCACTGTACTCG [G/A]GGAAAGTTG GGGATTTACCCGT AGT	G	A	Pro	Pro	SILENT- CODING	phosphoryla se	Human Gene SWISSPROT- ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.40E-155	

102	cg43996195	1421	TTGCAACTTGAGG TCGGTGCCTTAGT G/AJTGAGACAGAA GCCATTCTGCAGT GT	G	A	His	His	SILENT- CODING	phosphoryla se	Human Gene SWISSPROT- ID: P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.40E-155	
103	cg43948227	372	TTTACAGTTTTCCT ACTGCATCATC(A/ T)ATGTCAGAAATC TGTTCCCTCAGCT	A	T	Ile	Ile	SILENT- CODING	polymerase	Human Gene Similar to SWISSNEW- ID: P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa. pcis: SWISSPROT-ID: P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5

104	cg43333426	1302	AGAGCCACTACAA GGTGACTACTC A/GJCGTTTCACA AGACCTACGAGG TGG	G	Ser	Ser	SILENT- CODING	potassium_ channel	Human Gene SWISSNEW- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.40E-241	
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105	cg43051431	1683	TCACACCTGTCCT GACCCCTGGAGGA T/C/GGGTTCTACG AAGTTGACTACAA CA	T	C	Asp	SILENT- CODING	potassium_ channel	Human Gene SWISSPROT- ID:P48051 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 2 (GIRK2) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 6) (KATP-2) (BIR1) (KIR3.2) - HOMO SAPIENS (HUMAN), 423 aa. pcids: TREMBLNEW-ID: G1518526 INWARDLY RECTIFYING POTASSIUM CHANNEL KIR3.2 - HOMO SAPIENS (HUMAN), 423 aa.	1.60E-227	16
106	cg43920929	1081	GCAGGATCACCT GCACCCCTCTGG G[C/G]ACCATGAT GCTCATCCAGCTG TCTA	C	G	Val	SILENT- CODING	proteaseinhi b	Human Gene SWISSPROT- ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
107	cg43059041	624	AGTCAGACACCA GCTTAGAAATGAC [C/T]ATGGGCAAT GCC TTGTTTCTTG ATG	C	T	Thr	SILENT- CODING	proteaseinhi b	Human Gene Similar to SWISSPROT-ID:P17475 ALPHA-1- ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA- 1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83	14 (14q32.1)

108	cg40148056	1385	GGAGGACAGGCA ACTCATCACCAGAA [C/T]TAGTCATCAG CAAGATGAACCCAG CT	C	T	Leu	Leu	SILENT- CODING	struct	Human Gene SPTREMBL- ID:Q92777 SYNAPSIN IIB - HOMO SAPIENS (HUMAN), 478 aa.	2.90E-260	3 (3p)
109	cg42894986	1002	ACCCGTTCTTCTG CCCACCCACTGA[G/A]GCCCCAGAC CGTGACTTCTTGG TGG	G	A	Glu	Glu	SILENT- CODING	struct	Human Gene SPTREMBL- ID:Q28686 50-KDA DYSTROPHIN- ASSOCIATED GLYCOPROTEIN PRECURSOR - ORYCTOLAGUS CUNICULUS (RABBIT), 387 aa.	1.40E-180	17
110	cg43961212	2160	TCTGGAAGCCGG ACATCCTCTGAGC [A/G]AGTCGACTG ATCCGCTGGCGA ACCA	A	G	Leu	Leu	SILENT- CODING	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 261 aa.	2.40E-114	
111	cg42898003	497	TCATCAGAGATTG GATCTCCTCGTC[C/A]GTCACGTGCT CCCCGGAGGCCCC TGA	C	A	Thr	Thr	SILENT- CODING	struct	Human Gene Similar to SWISSPROT-ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.50E-80	20 (20q12)
112	cg43960684	788	GCTTTGAGGAGG AGGCGCGGTTGC G[C/G]GACGACAC TGAGGCGGCCAT CCGCG	C	G	Arg	Arg	SILENT- CODING	struct	Human Gene Similar to SWISSPROT-ID:P02535 KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (56 KD CYTOKERATIN) (KERATIN, TYPE I CYTOSKELETAL 59 KD) - MUS MUSCULUS (MOUSE), 569 aa.	8.30E-58	8

113	cg43958714	1049	TTCGGAAAGGGC AAGCAGTGACCCT [G/C]ATGATGGAT GCCACCAATATGC CAG	G	C	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SPTREMBL- ID:Q42761 SQUALENE SYNTHASE (EC 2.5.1.21) (FARNESYL- DIPHOSPHATE FARNESYLTRANSFERASE) (FARNESYLTRANSFERASE) (PRESQUALENE-DI- DIPHOSPHATE SYNTHASE) - GLYCYRRHIZA GLABRA, 412 aa.	9.20E-83	8
114	cg43124627	901	ACACCCACAGCA GTTTGGTTTAGG] A/T]TATCTGTAAA TGGAAGGTTCTG GC	A	T	Gly	Gly	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16

CG43968419 906 TCTTCTCCAACAG A T Ala Ala

115	cg43968419	906	TCTTCTCCAACAG TCTGCCACCCGCT A/TJGTGTTGGCT GCGCCCTCCAAGG CCC	A	T	Ala	Ala	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P53556 8-AMINO-7- OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO- PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE- -PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.jpclis:SWISSPROT-ID:P53556 8- AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO- 8-AMINO- PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE-- PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.	9.90E-70	
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116	cg43064068	1484	TTGTGGTCCTGGC CTCGCAGTTCTT G/AJTCCTCCATGACC CAGAACAGCTCAC CA	G	A	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
117	cg43064068	1622	TCACAGGGAAT TCAACGAGCCAA G/AJCTTCGAGACA AGGAGTGAAGA TGT	G	A	Lys	Lys	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	

118	cg41084924	1278	TGACTCTCCCCGA CCCGTCCCACCA C/TGGTCTCCACA GCACTCCCGACA GCC	C	T	His	His	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
119	cg41084924	1662	TCCGCAAGGCCTT CCTGAAGATCCTT C/TCACTGCTGAC TCTGCTGCCTGCC CG	C	T	Leu	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
120	cg41084924	606	TCCTCGTCGCCAC ACTGGTCATGCC C/AJTGCGTGTCT ACCTGGAGGTGG TAG	C	A	Pro	Pro	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	
121	cg43985000	1471	TTGCTCTTTGCTG GTTCCCTCTTCA /JTAAAGCCGTAT ATTGAAGAAA G	C	T	His	His	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
122	cg43985000	1507	TATTGAAGAAAAC TGTTGATAACGA /GJATGGACAAGAA CCGATGTGAATTA C	A	G	Glu	Glu	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4

123	cg44930578	561	ACGTGAACACCG ACATCTACTCCAA[G/A]GTGCTGGTGA CCGCCGTGTACC TGG	G	A	Lys	Lys	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P30989 NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1) (HIGH-AFFINITY LEVOCABASTINE- INSENSITIVE NEUROTENSIN RECEPTOR) (NTRH) - HOMO SAPIENS (HUMAN), 418 aa.	5.00E-217	
124	cg3003519	1263	ATTCCTTGATTGC TAGGACCCCTTTA[C/T]TAAAGCACCC TGAACATACCTAC TG	C	T	Tyr	Tyr	SILENT- CODING	tm7	Human Gene SWISSNEW- ID:P32247 BOMBESIN RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.lpcis:SWISSPROT-ID:P32247 BOMBESIN RECEPTOR SUBTYPE- 3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.lpcis:TREMBLNEW-ID:E1240254 BOMBESIN RECEPTOR SUBTYPE- 3 (UTERINE BOMBESIN RECEPTOR, BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.	3.00E-212	X

125	cg3003519	711	CTTATGCTGTGAT CATTTCAGTGGG[C/TATCCTTGGAA ATGCTATTCTCAT CA	C	T	Gly	Gly	SILENT- CODING	tm7	Human Gene SWISSNEW- ID:P32247 BOMBESIN RECEPTOR SUBTYPE-3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.lpcis:SWISSPROT-ID:P32247 BOMBESIN RECEPTOR SUBTYPE- 3 (BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.lpcis:TREMBLNEW-ID:E1240254 BOMBESIN RECEPTOR SUBTYPE- 3 (UTERINE BOMBESIN RECEPTOR, BRS-3) - HOMO SAPIENS (HUMAN), 399 aa.	3.00E-212	X
126	cg43969010	1182	TCCGAAAGAAGTC TTGGGAGGTGTA[C/TTCAGGGAGTGT GCCAGAAAGGGG GCT	C	T	Tyr	Tyr	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P30411 B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR) - HOMO SAPIENS (HUMAN), 391 aa.	9.00E-211	12 (14q32.1)
127	cg43263108	1097	AGACACCCCTTTTC CCAGCTCGCCTC[C/AJGGGAGGAGG GACCCAAAGGGCC CCCT	C	A	Ser	Ser	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR) - HOMO SAPIENS (HUMAN), 386 aa.	8.30E-208	19 (19q13.3)
128	cg43263108	272	GCCCCCTCGGCCT TCGCGGTGCTGG TTC/GJACCGGACT GGCGGCCACCGA CCTGC	C	G	Val	Val	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P43119 PROSTACYCLIN RECEPTOR (PROSTANOID IP RECEPTOR) (PGI RECEPTOR) - HOMO SAPIENS (HUMAN), 386 aa.	8.30E-208	19 (19q13.3)

129	cg43267238	1220	CCAGACTGGTCCT GGTGGTGGTGGC[A/G]GTCTTCGTCG TCTGCTGGACTCC CA	A	G	Ala	Ala	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
130	cg43267238	392	CAGCACTCACCAT GGAATCCCCGAT[C/T]CAGATCTTCC GCGGGGAGCCCGG GCC	C	T	Ile	Ile	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
131	cg43267238	413	CGATCCAGATCTT CCGCGGGGAGCC [G/T]GGCCCTACC TGCGCCCCGAGC GCCT	G	T	Pro	Pro	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P41145 KAPPA-TYPE OPIOID RECEPTOR (KOR-1) - HOMO SAPIENS (HUMAN), 380 aa.	2.10E-204	8 (8q11.2)
132	cg43264978	155	TGGATCTGCACCT CTTCGACTACTC[A /C]GAGCCAGGGA ACTTCTCGACAT CA	A	C	Ser	Ser	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
133	cg3001696	1154	CGCTGCACCTGT GCATCGCGCTGG G[C/T]TACGCCAAT AGCAGCCTCAAC CCCCG	C	T	Gly	Gly	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195	1 (1p36.1)

134	cg3001696	815	TGGCTGTGACCC GTCCCCGGGACG G[G]TJGCAGTGGT GTGCATGCTCCA GTTCC	G	T	Gly	Gly	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195	1 (1p36.1)
135	cg42704646	407	TGGCCTTCCCGAT CACCATGCTGCTI C/G]ACTGGTTTCG TGGGCAACGCAC TGG	C	G	Leu	Leu	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.10E-194	1 (1p31.2)
136	cg43326635	347	GGGATGCCACCT TCTGCTTCATCGT C/G]TCGCTGGCG GTGGCTGATGTG GCCG	C	G	Val	Val	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
137	cg3003708	358	CCATCTCCTTCTG TGGCTGTCTCACI A/G]CAGATGTATT TCGTTTTTCATGTT CG	A	G	Thr	Thr	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160	
138	cg3003708	787	GGTGGAAAGCCT TCTCCACCTGTGG [I/C]TCTCACCTGG CTGTGGTTCTCCT CT	T	C	Gly	Gly	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160	

139	cg3003708	841	ACAGCACCATCAT TGCTGTGTATTTT /CJAACCCCTCTGTC CTCCCACTCAGCT G	T	C	Phe	Phe	SILENT- CODING	tm7	Human Gene TREMBLNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160	
140	cg36729339	537	ACTCTCCAATGTA CTTTTCCTCTC[C /TAAACCTCTCCTT CTTGGACCTCTGC T	C	T	Ser	Ser	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:Q15062 OLFACTORY RECEPTOR-LIKE PROTEIN FAT11 - HOMO SAPIENS (HUMAN), 316 aa.	1.90E-153	
141	cg38841806	717	GACATCAGGCGC ACGGTGCCCAACC T[C/G]CGCCATCT GCAGGCCCAAGAA GAAGT	C	G	Leu	Leu	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
142	cg38841806	723	AGGCGCACGGTG CCAACCTCCGCC A[T/C]CTGCAGGC CAAGAAGAAGTTT GTGA	T	C	His	His	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
143	cg38841806	96	CAGCCTTCTCCAT GCCCAGCTGGCA[G/A]CTGGCACTGT GGGCACCCAGCCT ACC	G	A	Gln	Gln	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	

144	cg43040273	1966	CCTGTGCTGATCT GGTCATGGGCCTT G/AJGCAGTGGTG CCCTTTGGGGCC GCCC	G	A	Leu	Leu	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
145	cg43040273	2237	CTTGCCCATTCAG ATGCACTGGTACI C/AJGGGCCACCC ACCAGGAAGCCA TCAA	C	A	Arg	Arg	SILENT- CODING	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
146	cg43336100	687	TTGGAAGCGTGC ATCCAGTGAGACC [A/T]ATGAGGCTTG AGTCITTTTAGTGC CT	A	T	Pro	Pro	SILENT- CODING	tnf	Human Gene SWISSPROT- ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	5
147	cg21646034	376	GTGTGAGCAGAG ATGCCAGAACCAG [A/GJGTGGACCGA ACACCATTACATA TGG	A	G	Lys	Lys	SILENT- CODING	transcriptfac tor	Human Gene SWISSPROT- ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9.00E-179	15

148	cg43916882	1608	TGGCAGCTACCA GCACACTGCCTC C/A/GICCGTCAAT AAAGGCACGTGATG GTCT	A	G	Gly	Gly	SILENT- CODING	transferase	Human Gene SWISSPROT- ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.30E-245	1
149	cg2537639	294	TGGCTCCCATTTGT CTGGGAGGGCAC[A/G]TTCAACATCG ACATCCTCAACGA GC	A	G	Thr	Thr	SILENT- CODING	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYLTRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	34

152	cg2537639	768	GGCCCCAGTCCC AGGCCTACATCCC [C/T]AAGGACGAG GGCGATTTCTACT ACC	T	Pro	Pro	SILENT- CODING	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYL TRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
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153	cg2537639	927	ACGAGAGCCACC TGAACAAGTACCT [G/A]CTGCGCCAC AAACCCACCAAG GTGC	G	A	Leu	Leu	SILENT- CODING	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYL TRANS- FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
154	cg44000740	732	GGGAGATACTG GCTCACCAGGA A[A/C]ACAGGGAA CATCACCTTATGC CACA	A	C	Val	Val	SILENT- CODING	transferase	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS- THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.60E-117	16


155	cg38869466	1185	ACGACGTGCGCG TGGCTCCCTCT G/C/TGGCTCTTCC GCCAGTCTTCTAG GTT	C	T	Cys	Cys	SILENT- CODING	transport	Human Gene SWISSPROT- ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa.	0	13
156	cg40351913	1347	CCATCGCCACGC TCCCTCTGTCCTC TAGGCGCTGGGCC GTGGTCTTCTTCA TCA	A	G	Ser	Ser	SILENT- CODING	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	15p15.3
157	cg43964039	1719	GATGGAACAGCT CCTCGGTGTCTT [G/A]TCACITTTGGC TGGCTCCCCCCT GCC	G	A	Asp	Asp	SILENT- CODING	transport	Human Gene SWISSPROT- ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
158	cg43992017	1656	GCGGCTGCTGGT GGATGGGTGGGC G/C/G]GGGGTGCA GCCTCCACCCCC TCCCC	C	G	Pro	Pro	SILENT- CODING	transport	Human Gene SPTREMBL- ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.40E-241	

159	cg43948629	1238	CGCCTGTAATGG CTGTGAACATGCT [C/T]ACCCAGCAG GAGGTCCTGTC GTTA	C	T	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q15031 PROBABLE LEUCYL- TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0	3
160	cg43955093	2875	CATTGACTAGGG GCTGTGGGGCA TTC/GCGCCAGG TGTCCTCCATCA GAGG	C	G	Arg	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
161	cg43955093	3385	AGCAGGCCAAGA GAGATCTGTGGAA [C/T]GCATCTTGT CCAGAAATACCAGA TA	C	T	Ala	Ala	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
162	cg43055918	517	CGCTGGCATAGG ACATGGCGGGCT T[G/T]CCCCCGC AGAGCTCTGGGG GCTAC	G	T	Gly	Gly	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
163	cg43974592	254	AAATAACAAGGCA TTGAAGAAATGGC[T/A]GACGAGCGG AAAGACGAAGGA AAGG	T	A	Ala	Ala	SILENT- CODING	UNCLASSI FIED	Human Gene REMTREMBL- ACC:E1296438 SEQUENCE 28 FROM PATENT WO9727323 - UNIDENTIFIED, 1829 aa.	0	2 (2q34)

164	cg43956384	206	AAGGACGCAACG CTGCCACCATGG A/C/TAGTAGCAC CTGGAGCCCCAA GACCA	C	T	Asp	Asp	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)
165	cg44025634	2757	TGAAAGTATTCAA TCCCAGAAAGGAA A/G/CTGGAATTG CCCTTCTGTTCT AG	A	G	Lys	Lys	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSNEW- ACC:P00450 CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE) - Homo sapiens (Human), 1065 aa.	0	3 (3q21)
166	cg43940037	2472	GCTGGGCGCACTG CTAGCCTCAGAG G/T/A/GCCAGCAC CTCCTCAGCCCC CGCGC	T	A	Ala	Ala	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P41250 GLYCYL-TRNA SYNTHETASE (EC 6.1.1.14) (GLYCINE--TRNA LIGASE) (GLYRS) - Homo sapiens (Human), 685 aa.	0	7 (7p15)
167	cg44024279	481	AAAACCAGCTACC TGCCCTTCTGGA A/G/GAACTTTGCC ATGAGAAAGAAAT TT	A	G	Glu	Glu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P02771 ALPHA- FETOPROTEIN PRECURSOR (ALPHA-FETOglobulin) (ALPHA- 1-FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	

168	cg43926814	1122	CATGAGTTTGTGAT CCAGCTCTTCTI C/TTCCTGGCTT TCTGGGCCATTTCTC	C	T	Glu	Glu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa.	5.00E-289	14
169	cg40918088	1778	TTGGAGCTGGAAT TACTGTGTATGAJA /GJCCCTTAGCAGC TGCTGATGAGCTT T	A	G	Glu	Glu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.80E-287	X (Xq28)
170	cg43966985	1242	TCAACACCTACGT CCACTTCCAAGGJ G/TJAAGATGAAGG GCTTCTCCCTGCT GG	G	T	Gly	Gly	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P01019 ANGIOTENSINOGEN PRECURSOR - Homo sapiens (Human), 485 aa.	3.90E-257	1 (1q42)
171	cg43924009	770	TGGCTTGCACAAA TTGCTTGAAGACJ ATTCGATCCATGT AAGTGGA CTGTCT TG	A	T	Arg	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:O43411 HYPOTHETICAL 49.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 442 aa (fragment).	6.90E-239	
172	cg42913861	2186	CTGGGCAGCTGC CCTCACAGTAGTT [C/G]CCG TAGTAG CCGGTGGGTGCT ATGA	C	G	Gly	Gly	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227	2 (2cen)

173	cg42913861	2354	GCCGAGCCTGCA CCACCACAAAGG G[C/T]CGGTGCGA CTCTTCGCCTGG GTCCA	C	T	Arg	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227	2 (2cen)
174	cg43929685	256	CATAGAAAGGCCA GGAGTCAGGAGA C[C/T]TGGGTTCT GTCCTGGATTATA CACC	C	T	Gln	Gln	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P29080 (2'- 5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) ((2- 5')OLIGO(A) SYNTHETASE 1B) (2- 5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.40E-225	12
175	cg43929685	268	GGAGTCAGGAGA CCTGGGTTCTGTC [C/T]TGGATTATAC ACCAGCTCACTGA GG	C	T	Gln	Gln	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P29080 (2'- 5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) ((2- 5')OLIGO(A) SYNTHETASE 1B) (2- 5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.40E-225	12
176	cg43918561	53	CCATGCCCACCC CCGACGCCACCA C[G/C]CCACAGGC CAAGGGCTTCCG CAGGG	G	C	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.10E-224	11 (11p15.5)

177	cg42343176	1885	ATTTAATGAATTC CTGAAGACTGT[A] GJAGAAGTACAAC TGAGAAATCCCTT T	A	G	Val	Val	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P14902 INDOLEAMINE 2,3- DIOXYGENASE (EC 1.13.11.42) (IDO) (INDOLEAMINE- PYRROLE 2,3-DIOXYGENASE) - Homo sapiens (Human), 403 aa.	3.90E-218	8 (8p12)
178	cg43956382	1146	AAAACAATGATAT CGATGAAGTTAT[C/T]ATTCCACAG CTCCCTTATACAA AC	C	T	Ile	Ile	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q99816 TUMOR SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 390 aa.	4.90E-211	11 
179	cg43984681	979	CACCATGAAGCA GTTGCTGCGGGC C[C/T]TGGAGGAG GGCCGCGTGCGG GAAGT	C	T	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.30E-210	12 (19q13)
180	cg43984681	1074	TCCTGTACAAAGA CAGGAACCTCCA[C/T]ATTCCACCA TGGAAATGGGC CTG	C	T	His	His	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.30E-210	19 (19q13)

181	cg43950996	1762	CTGCGGTGGAGA CGTCAGAGCTGC C/A/G/GGGGAGGG GGCTCCTGCGCC ACAGC	A	G	Pro	Pro	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.20E-204	1
182	cg44024506	988	ACCAGCTGCTCGT AGTACACAGGCA G/A/GCACCTCTCC TTGCCTACCTCCA TG	G	A	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:O60704 TYROSYLPROTEIN SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 377 aa.	1.90E-200	22
183	cg43980381	1114	CTACCGCCAACTA TGACTTTGTCCCTC /GJAAGAAGCGGA CCTTCACCAAGG GAG	C	G	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.60E-191	

184	cg42650960	501	TCCCCTGGCAGA ACTACCACCTGAA [C/T]GACTGGATG GAGGAGGAATAC CGCC	C	T	Asn	Asn	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:Q10981 GALACTOSIDE 2-L- FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L-FUCOSE:BETA-D- GALACTOSIDE 2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA-2- FUCOSYLTRANSFERASE) (SECRETOR FACTOR) (SE) (SE2) - Homo sapiens (Human), 343 aa.	2.00E-189	
185	cg43249389	1497	ACATCCAGGTGGT GTTTCGACGCCGT C/T]ACCGACATCA TCATTGCCAACAA CC	C	T	Val	Val	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
186	cg43946951	615	CAGTGACGGCAG GGTCAAAGTCCTT [G/A]GCGTAGCCC TCGTTAAGGCTGT AGA	G	A	Ala	Ala	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09467 FRUCTOSE-1,6- BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6- BISPHOSPHATE 1- PHOSPHOHYDROLASE) (FBPASE) - Homo sapiens (Human), 337 aa.	3.50E-178	9 (9q22.2)

187	cg43248117	1054	AACCAGCCCCACT GTGAGAAAGACCA C/G/C]GTGTTCAA GTCTTTGGGAATG GCAG	G	C	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSPROT- ACC:Q14894 MU-CRYSTALLIN HOMOLOG (NADP-REGULATED THYROID-HORMONE BINDING PROTEIN) - Homo sapiens (Human), 314 aa.	1.20E-161	16 (16p13.1 1)
188	cg44027049	482	CCACAATGTTAGG AGGGTATTTTA[C T]ATCCCTCCAGT TAACAAATACAGC A	C	T	Tyr	Tyr	SILENT- CODING	UNCLASSI FIED	Human Gene SWISSNEW- ACC:P11245 ARYLAMINE N- ACETYLTRANSFERASE, POLYMORPHIC (EC 2.3.1.5) (PNAT) (NAT-2) (ARYLAMINE ACETYLASE) - Homo sapiens (Human), 290 aa.	5.40E-157	8 (8p23.1)
189	cg43982075	499	CTGCCATCTTTCA GCCCTCTGAAACI C/T]GTGTCAGCA CAGAATCTTCCCT GG	C	T	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q15729 THYROTROPH EMBRYONIC FACTOR - HOMO SAPIENS (HUMAN), 303 aa.	1.20E-154	22
190	cg43942977	350	GCGCTTCCCAGG TCCGGACAAATTCG [G/T]CAGACTATTG TCAAACTGGGGAA TA	G	T	Arg	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	
191	cg43942977	701	GGCAGCTGAAGA TCACCAATGCTGG [G/C]ATGGTGCT GATGAGGAGTTG GAGC	G	C	Gly	Gly	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	

192	cg43942977	773	GCGAGGTGTTTGT GTCCAATATCCTT GTTAAGGACACGC AGGTGACTCGAC AGG	G	T	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	
193	cg43985220	753	TGTACACTGCCAG AAAAGGAAAAGG T/GGCCCTTTTGT ATGGTCAAAAAC AC	T	G	Gly	Gly	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.10E-145	8
194	cg43985220	837	TCTTGGTGACTGA GTTGGGCTCTTC C/TJAGAACACCCAG AGACTGTGAGAAT GG	C	T	Ser	Ser	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.10E-145	8
195	cg43946394	321	TAGAGCGCACAC AGGCCCTCCAGCT G/A/GJGCCATGTC CGTCTCATCATCC CAAG	A	G	Ala	Ala	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1-DELTA) - Homo sapiens (Human), 281 aa.	2.80E-144	19

196	cg43119818	1329	CTGACAGCTACAG GCTCTTTTCAGTTTC TTTCATTTTCACTG GGGCAGTACAAAT G	C	T	Phe	Phe	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P0915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.90E-141	8 (8q22)
197	cg43118279	735	AGAAGTTGAAGG GGCTGGTGCCAC TTT/GGGACCCGA ATCAAGTCGACAC ACTA	T	G	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:Q05195 MAD PROTEIN (MAX DIMERIZER) - Homo sapiens (Human), 221 aa.	1.20E-111	2 (2p13)
198	cg43325007	866	TGGGTTGAGGA TGAGCCCTTCTC TTT/CACAGCCAGG CGGCTCAGGGCA AACA	T	C	Val	Val	SILENT- CODING	UNCLASSI FIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
199	cg39524111	402	GCCAAATATAGGAT AGGGCACTACAG[A/G]TTCCGGTACA GTGACACCCCTGG AGC	A	G	Arg	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:BAA13472 CD89_U08 - HOMO SAPIENS (HUMAN), 191 aa.	2.10E-100	19 (19q13.4)
200	cg43280516	629	ACGGGAGGAGC TGCAGATGGAAC C/C/TGTGTGAGG TGTCCTCTGGGAC CTGC	C	T	Pro	Pro	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.80E-95	19

201	cg43963913	871	AGAGGTTGGGG GCGCCGAGCGCG A[G/A]CGGCCCG AAAGGGGCTGGG CTCCT	G	A	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.10E-90	11
202	cg40262905	682	TAGTGAAGGCCT GAAATATATGCTG /C]GAGGTGGAAT TGGCAGAACTACC T	G	C	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:BAA34941 HUMAN CMAP - HOMO SAPIENS (HUMAN), 167 aa.	1.30E-89	
203	cg43918168	915	CTCCATCAACAGC ATCCGGACTGCA[T/C]GGCGGCTCG CCGTGCGGCTGG GGCC	T	C	Pro	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	3.80E-85	(12q23)
204	cg43259701	136	CGACGAGGTGCT ACGCGAGGGCGA G[C/T]TGAGAGAG CGCAGCGACAGC CTCTT	C	T	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O00496 IPL (IPL) - HOMO SAPIENS (HUMAN), 152 aa.	1.30E-77	11
205	cg1527767	162	TTTTTCCAGCTT ACAATGGTACAG[A/G]CAGGAGCCT GGGGAAGGTCCT GTCC	A	G	Arg	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G36907 T-CELL RECEPTOR ALPHA-CHAIN HAP58 V(A)10.1-J(A)T - HOMO SAPIENS (HUMAN), 135 aa (fragment).	5.60E-68	

206	cg40968986	316	AGAAGAGAGCCT GTGACACTGCCA C/C/TGTGTGACT CATCGGCTGGCA GGCT	C	T	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
207	cg42550133	300	TCATCCTGAGTTC TAAGAAAGCTCC[T /C]CTCAGTGACTC TGGCTTCTATCTC T	T	C	Leu	Leu	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:D1002898 T- CELL RECEPTOR BETA-CHAIN V REGION - HOMO SAPIENS (HUMAN), 112 aa (fragment).	8.50E-56	7 (7q35)
208	cg2526759	317	CTCTGGTTGTCCA CGAGGGAGACAC[T/C]GTAACCTCTCA ATTGCAGTTATGA AG	T	C	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	
209	cg41664708	249	AAGTCTGTGCTGA TCCACAAGCCAC[A/G]TGGGTGAGA GACGTGGTCAGG AGCA	A	G	Thr	Thr	SILENT- CODING	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2.00E-54	1
210	cg43300673	1571	AGGAGGCGGGG AGGGTAGCATGG G[G/gap]CACACGG CCCTCACAGGGA CTCACT	G	gap			SILENT- NONCODI NG	ATPase_as sociated	Human Gene SPTREMBL- ID:Q93050 VACUOLAR-TYPE H(+)- ATPASE 115 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 831 aa.	0	17

211	cg43284434	2570	AGTTGAAATCAGA GAGGAATAAAAA[ap/A]GACATTTTAT ATTTTATTCTGCT CC	gap	A				SILENT- NONCODI NG	ATPase_as sociated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
212	cg43132502	196	TAAGCATGAGGTG GCACGAGGCAGG[A/C]GTTGGCGATG CCACCTGGGGGT CAC	A	C				SILENT- NONCODI NG	ATPase_as sociated	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
213	cg43931765	606	GGTCCCTTGCTT TATCCCAAGCTC[G/T]GAGGGACGC AGCCTGGCATGG CTCT	G	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	
214	cg43931765	607	GTCCCTTGCTTT ATCCCAAGCTCG[G/T]AGGGACGCA GCCTGGCATGGC TCTG	G	T				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
215	cg43931765	615	CTTATCCCAAGC TCGGAGGGACGC[gap/G]AGCCTGGC ATGGCTCTGGCCT AGCA	gap	G				SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3

216	cg43931765	660	TAGCAGCCAGGT GACATGGCCAGG C[gap]/TACCTTCC TGACAGGCACTG TGGGC	gap	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
217	cg43931765	665	GCCAGGTGACAT GGCCAGGCACCT T[gap]/TCTGTAC AGGCACTGTGGG CTCCTG	gap	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
218	cg43931765	668	AGGTGACATGGC CAGGCACCTTCCT [gap]/TGTACAGG ACTGTGGGCTCCT GGCC	gap	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
219	cg43931765	668	AGGTGACATGGC CAGGCACCTTCCT [gap]/TGTACAGG ACTGTGGGCTCCT GGCC	gap	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
220	cg43931765	668	AGGTGACATGGC CAGGCACCTTCCT [gap]/TGTACAGG ACTGTGGGCTCCT GGCC	gap	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3

221	cg43952088	4769	AATCCACAATCGG CATCAGGAAGCC[A/C]AAGTCCAGT GGCCATTAGGGT CCT	A	C			SILENT- NONCODI NG	cadherin	Human Gene SPTREMBL- ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0	16
222	cg44010957	1406	TCCCTATGAGCCT GCAAAGGAGACA[G/T]TCAGGAATGA GTTCCATGTTCTCGA GA	G	T			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P20701 LEUKOCYTE ADHESION GLYCOPROTEIN LFA-1 ALPHA CHAIN PRECURSOR (LEUKOCYTE FUNCTION ASSOCIATED MOLECULE 1, ALPHA CHAIN) (CD11A) (INTEGRIN ALPHA-L) - HOMO SAPIENS (HUMAN), 1170 aa.	0	16 (16p11.2)
223	cg43956560	1463	CAGTGCACTCTGG GAAGATTTCTACCC[T/C]GACCAACAGT TCCTTCAGCTTCC AT	T	C			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1,00E-218	1 (1q23)

224	cg43956560	1492	CAACAGTTCCTTC AGCTTCCATTTC[G /A]CCCCCTCATTTA TCCCTCAACCCCC A	G	A			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)
225	cg43956560	2242	TGCTCTCCITTC CCTGCCCCAGAG C/A]CTTTTATCCA CTTACCTAGATTC TA	C	A			SILENT- NONCODI NG	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)

226	cg43264626	428	TGCCACAGTGA AAAAGGTCATGG GTTA]GGAGAGAA GCAAAGTAGGAA GGATC	T	A			SILENT- NONCODI NG	cathepsin	Human Gene SWISSPROT- ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
227	cg43011543	1972	ACCGCACCCCTTC CACCGGTGGGG [C/G]CCCAGTGAA GTTTAACAAACTG CTG	C	G			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT- ID:P27658 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
228	cg43011543	2096	CATACCACGTTCA CTGCAAGGGGGG[C/G]AACGTGTGG GTTGCTCTATTCA AGA	C	G			SILENT- NONCODI NG	collagen	Human Gene SWISSPROT- ID:P27658 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
229	cg43933757	2546	GAAACCCAGTAG GCTCCTGGAGGC C/A/C]TGGTCAGC TTGCTTGAATCC AGCA	A	C			SILENT- NONCODI NG	complement	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
230	cg41553795	64	TGGTGGTGCTAC CCTTGGCCCTCCCA [C/G]AGTCCTGCC ACCCTGCTGCCG CCAC	C	G			SILENT- NONCODI NG	complement	Human Gene Homologous to SWISSPROT-ID:P07360 COMPLEMENT C8 GAMMA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 202 aa.	1.40E-104	9 (9q34.3)

231	cg42542496	168	AGCCCTTCTCCAC CCGGATAGATTCT C/TTCACCCCTTGG CCCGCCCTTTGCC CCA	C	T			SILENT- NONCODI NG	csf	Human Gene SWISSPROT- ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
232	cg42542496	179	ACCCGGATAGATT CCTCACCCCTTGGI C/TCCGCCCTTTGC CCCACCCCTACTCT GC	C	T			SILENT- NONCODI NG	csf	Human Gene SWISSPROT- ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
233	cg41533258	1356	GTGCCTGGACATT TGCCTTGCTGGA C/TGGGGACTGG GGATGTGGGAGG GAGC	C	T			SILENT- NONCODI NG	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY- STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPROTEIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107	17 (17q11.2)

234	cg2753430	657	ACGACTTTGAGCC TCGCGATCTTTT[g ap/G]AGTCCAACG TCCAGCTCGTTCT CTG	gap	G			SILENT- NONCODI NG	csf	Human Gene Similar to SWISSNEW- ID:P08700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY- STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF) - HOMO SAPIENS (HUMAN), 152 aa.lpcis:SWISSPROT-ID:P08700 INTERLEUKIN-3 PRECURSOR (IL- 3) (MULTIPOTENTIAL COLONY- STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF) - HOMO SAPIENS (HUMAN), 152 aa.	1.10E-77	5
235	cg44036323	225	TGCGGCTTAAAG GGCAACCCGCGC[G/C]GGACCCCTTCC TCCCTAGTCGCG GGG	G	C			SILENT- NONCODI NG	dehydrogen ase	Human Gene SWISSPROT- ID:P00367 GLUTAMATE DEHYDROGENASE 1 PRECURSOR (EC 1.4.1.3) (GDH) - HOMO SAPIENS (HUMAN), 558 aa.	5.80E-303	10

236	cg43918671	766	GAGAGACCATTTA CTTACATCAGTT[C /T]GGTTTATAGAC ATTTGAATCATAT C	C	T			SILENT- NONCODI NG	dehydrogen ase	Human Gene SPTREMBL- ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.10E-272	7 (7q31)
237	cg43057018	1995	AGTTTCATTATAC TTTTCTCTCCACig ap/GJTTTTGTCTAT GTTGAAAATTTTC TG	gap	G			SILENT- NONCODI NG	dehydrogen ase	Human Gene SWISSNEW- ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.lpcis:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
238	cg44005808	3691	ACAAGACAGAG CTGAAGTGCAATCC [gap/C]AAAGGTGC TCAGAGAGCCCGG CCCCGC	gap	C			SILENT- NONCODI NG	dna_ma_bi nd	Human Gene SWISSNEW- ID:P19838 NUCLEAR FACTOR NF- KAPPA-B P105 SUBUNIT (DNA- BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) - HOMO SAPIENS (HUMAN), 969 aa.	0	

239	cg44005808	630	TCTTCCTTCTCCA GCCGGCAGGCCC [gap/G]CGCCGCTT AGGAGGGAGAGC CCACC	gap	G			SILENT- NONCODI NG	dna_ma_bi nd	Human Gene SWISSNEW- ID:P19838 NUCLEAR FACTOR NF- KAPPA-B P105 SUBUNIT (DNA- BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa pcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) - HOMO SAPIENS (HUMAN), 969 aa.	0	
240	cg43956159	1244	TGGCGAGTCCAG GGTCACCCACATA [gap/A]CCATGCAC CACGGGTGCTAT GCCGC	gap	A			SILENT- NONCODI NG	dna_ma_bi nd	Human Gene SPTREMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
241	cg43956159	1248	GAGTCCAGGTC ACCCACATACCAT [gap/T]GCACCACG GGTGCTATGCCG CTTCT	gap	T			SILENT- NONCODI NG	dna_ma_bi nd	Human Gene SPTREMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10

242	cg43956159	1268	TACCATGCACCCAC GGGTGCTATGCC[G/A]CTTCTTACAG GACCTTTTATGCC CT	G	A			SILENT- NONCODI NG	dna_rna_bi nd	Human Gene SPTREMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
243	cg43956159	1342	CCTGGAGGCAAC TGGGTAGGGTGC A[G/C]AACGGCAT GCTTTGGCTGGAA CACG	G	C			SILENT- NONCODI NG	dna_rna_bi nd	Human Gene SPTREMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
244	cg43956159	1364	CAGAACGGCATG CTTTGGCTGGAAC [gap/C]ACGCATCC CTCCTTCCACGGC CGGC	gap	C			SILENT- NONCODI NG	dna_rna_bi nd	Human Gene SPTREMBL- ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
245	cg43971258	471	CAGAGCTAGCTCT GGCTCTTCAGGC[C/T]ACAAGTTCAC AGTCCTTCGCTCC TG	C	T			SILENT- NONCODI NG	dna_rna_bi nd_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX- LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa. lpcis:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)

246	cg43971258	508	GTCCTTCGCTCCT GAGCACCAGGTTT T/CJAGTCTCCAGG AAGGGATTGGTG AA	T	C			SILENT- NONCODI NG	dna_ma_bi nd_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX- LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa. lpcis:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60	1 (1p36.13)
247	cg43982507	3373	GATACCTTTGCGT GGATCAAGCTTG gap/CJTGACTTGA CCGTTTTATATTA CT	gap	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT- ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
248	cg43982507	3739	CAAAAAAATTTAT AAACTAATTTTG ap/GJTACGTATGA ATGATATCTTTGA CCT	gap	G			SILENT- NONCODI NG	eph	Human Gene SWISSPROT- ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
249	cg43982507	514	CCTCCTTCTCCCC CTTCCCTCCCT A/CJGCCCCCACCT TCTTCCTCCTTTC GG	A	C			SILENT- NONCODI NG	eph	Human Gene SWISSPROT- ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)

250	cg41554010	1371	CTGCCCTGCCAC CTGTCTGTCTGTC [gap]/TCCAAAGAA GTTCTGGTATGAA CTTG	gap	T			SILENT- NONCODI NG	eph	Human Gene SWISSNEW- ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.lpcis:SWISSPROT-ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203	11 (11q23)
251	cg41554010	1371	CTGCCCTGCCAC CTGTCTGTCTGTC [gap]/TCCAAAGAA GTTCTGGTATGAA CTTG	gap	T			SILENT- NONCODI NG	eph	Human Gene SWISSNEW- ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.lpcis:SWISSPROT-ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203	11 (11q23)
252	cg43984905	2376	TCCCTCCAGGACT AGGCTGGAGGAA[G/C]CCAGTGGGG TCCCCCCTGAGT GGGC	G	C			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT- ID:P51178 1- PHOSPHATIDYLINOSITOL 4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3

253	cg43984905	2440	CACATGTGGGGA CAGGGCTGGTGT G G C TGTCTCC AGCCTCTTGCTCA GAGC	G	C			SILENT- NONCODI NG	esterase	Human Gene SWISSPROT- ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-II) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
254	cg43992911	382	CTAAAGTCGGAGT ATCTTCTTCCAA[G /A ATTTACAGTCT TGCGGGCCGTTG CA	G	A			SILENT- NONCODI NG	glycoprotein	Human Gene SWISSPROT- ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0	7
255	cg43932434	267	TTTCTAGAGGGG GTCTGTTGAAGAT [G A TGTAACTAGT ACACCCCAACCC CCA	G	A			SILENT- NONCODI NG	glycoprotein	Human Gene SWISSPROT- ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-1) (EXTRACELLULAR MATRIX RECEPTOR-II) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)

256	cg43932434	306	CCCCAACCCCA ACCTCAGTGGAAA A/G CAATGCCCA GGGATTAGGCTAT GGA	A	G			SILENT- NONCODI NG	glycoprotein	Human Gene SWISSPROT- ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-1) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
257	cg43318219	366	GCGCAGGTCAGA GGCGGCGCCGAG C A/G GGCCTCCG CGAGGTCCCCAC GCCGG	A	G			SILENT- NONCODI NG	glycoprotein	Human Gene SWISSNEW- ID:P15813 T-CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa. pcis: SWISSPROT-ID: P15813 T- CELL SURFACE GLYCOPROTEIN CD1D PRECURSOR (CD1D ANTIGEN) (R3G1) - HOMO SAPIENS (HUMAN), 335 aa.	3.10E-185	1 (1q21)

258	cg43967861	1954	CTCTATACTGTAC ACTCACCCTAAAT /gap]TCAAACAATT ACACCATGGTATA AA	T	gap			SILENT- NONCODI NG	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	8.20E-67	2
259	cg43967861	1955	TCCTATACTGTACA CTCACCCTAAAT /gap]CAAACAATTA CACCATGGTATAA AG	T	gap			SILENT- NONCODI NG	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	8.20E-67	2
260	cg43965366	1411	GCCGAATAGCCT GGGTTTGGAAAA G[C/T]ATGTTTTTG AAATATGTGGGAT CTC	C	T			SILENT- NONCODI NG	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)
261	cg43965366	385	TACTGACCTAAAT CACACCCTAGAC A/T]ATCAGAGGG AAATTCTGACCAT AA	A	T			SILENT- NONCODI NG	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)

262	cg43322513	1255	TGTCCTTGAAGAA CATGCACCTTGGC[A/G]CGGATGGCA CAAGCAAAATGGT AGA	A	G			SILENT- NONCODI NG	glycoprotein	Human Gene Similar to SWISSPROT-ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
263	cg41637704	1397	CCCGCGCCCCAG TAGGAGCCCCGC G[gap]/G]CCCCAGCA GGTGCGGCGCGC ACGGAG	gap	G			SILENT- NONCODI NG	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
264	cg41637704	1423	CCAGCAGGTGCG GCGCGCACGGAG C[gap]/G]CGCCGG CCGGCGGCTTCT CCCGGAG	gap	G			SILENT- NONCODI NG	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
265	cg41637704	1817	TGAAACTTGAAC CGCCTCTGGAGC[C/T]GCCATTCTGC AGAGTATTGGAA AA	C	T			SILENT- NONCODI NG	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
266	cg43980506	939	TCCAAGAAAGGGT CATGGAAGCTTA[T/C]TGGGAATAAT CCTCTCAATTAGA AA	T	C			SILENT- NONCODI NG	homeobox	Human Gene TREMBLNEW- ID:G2896172 LIM HOMEBOX PROTEIN COFACTOR - HOMO SAPIENS (HUMAN), 373 aa.	1.60E-206	

267	cg43961305	100	GGGGGGTTTTTT TTTTTCTCTG/ TTTTTTTTTTTT TTTTTTTTTTTT	G	T			SILENT- NONCODI NG	hydrolase	Human Gene SWISSPROT- ID:P37980 INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE) - BOS TAURUS (BOVINE), 289 aa.	1.30E-156	10
268	cg43998672	503	CTGGGGTTTTTC GGGAGGAACCA A[G/gap]GGCTCAC GGAGCCTCCTGT GCTGCA	G	gap			SILENT- NONCODI NG	hydroxyster oid	Human Gene SPTREMBL- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
269	cg43998672	505	GGGGGTTTTTCGG GGAGGAACCAAG G[G/gap]CTCACGG AGCCTCCTGTGCT GCAGT	G	gap			SILENT- NONCODI NG	hydroxyster oid	Human Gene SPTREMBL- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
270	cg42908571	1031	GAGTTAATTTATG TAAGTCATATTTIg ap/TATATTTTAA GAAGTACCACCTTG AA	gap	T			SILENT- NONCODI NG	interleukin	Human Gene Homologous to SWISSPROT-ID:P05231 INTERLEUKIN-6 PRECURSOR (IL- 6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)

271	cg42908571	1178	CTTACCTCAAATA AATGGCTAACTTIG ap/TJATACATATTT TTAAAGAAATATTT A	gap	T			SILENT- NONCODI NG	interleukin	Human Gene Homologous to SWISSPROT-ID: P05231 INTERLEUKIN-6 PRECURSOR (IL- 6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) - HOMO SAPIENS (HUMAN), 212 aa.	3.40E-108	7 (7p21)
272	cg42164914	1617	CAGCCCCCATTGT GGTCACAGGAAGI T/CJAGAGGAGGC CACGTTCTTACTA GTT	T	C			SILENT- NONCODI NG	interleukinre cept	Human Gene SWISSPROT- ID: P25025 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL- 8R B) (CXCR-2) (GROMGSA RECEPTOR) (IL-8 RECEPTOR TYPE 2) - HOMO SAPIENS (HUMAN), 360 aa.	9.60E-191	2 (2q35)
273	cg43958501	1133	CCCAACCTGGGTT TGGCAGACATCAI A/GJAATGATGGAG TACATTTTGCAGA TA	A	G			SILENT- NONCODI NG	isomerase	Human Gene SWISSPROT- ID: P46926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6-PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.60E-156	5

274	cg43958501	805	CACCCCCAGGTT CTCCTAGTTCAGA [G/A]AAAAGCTGT GAAAGTGAAGA AGGA	G	A			SILENT- NONCODI NG	isomerase	Human Gene SWISSPROT- ID:P46926 PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE- 6-PHOSPHATE DEAMINASE) (OSCILLIN) (KIAA0060) - HOMO SAPIENS (HUMAN), 289 aa.	1.60E-156	5
275	cg43090990	2710	TTTATTCTATTCCT ATCTGTGGATGT/ GJGTAAATGGCTG GGGGGCCAGCCCC TG	T	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT- ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC- THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0	10
276	cg42879455	2259	AGCCTTTGTGCTC CCACTCAAATACAIA /C/JAAAGGCCCCCTC TCTACATCTGGGA A	A	C			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT- ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0	X (Xq21.3)

277	cg42879455	2283	AAAAAGGCCCTC TCTACATCTGGG A/G ATGCACCTCT TCTTTGATTCCCT GG	A	G			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT- ID:Q06187 TYROSINE-PROTEIN KINASE BTK (EC 2.7.1.112) (BRUTON'S TYROSINE KINASE) (AGAMMAGLOBULINAEMIA TYROSINE KINASE) (ATK) (B CELL PROGENITOR KINASE) (BPK) - HOMO SAPIENS (HUMAN), 659 aa.	0	X (Xq21.3)
278	cg43971741	2151	AGCAACTTGGCTG AGCCCCACTACA C/T ACAGAGAAAT CATCAACCTGACT TA	C	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL- ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
279	cg43971741	2200	TAAGAGTTTTCAA GATGTCAAACTT[C /A AGGCTGATCAG CAGATGGGATGT GA	C	A			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL- ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9
280	cg43971741	2451	TTTTTAAAAATCCA TCCACACACAT[ga p/T GGTAAATTAA GTATAAATTC TTT G	gap	T			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL- ID:Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN) - HOMO SAPIENS (HUMAN), 540 aa.	1.40E-290	9

281	cg43947749	1996	AACGTCGATTCCG ACCGTCCCAACCTT G/gap]GCCCCGCC CCTCCTACAGCTG TAAC	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT- ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
282	cg43947749	1997	ACGTCGATTCCGA CCGTCCCAACCTG] G/gap]CCCCGCC CTCCTACAGCTGT AACT	G	gap			SILENT- NONCODI NG	kinase	Human Gene SWISSPROT- ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.60E-267	19
283	cg44131752	1535	CACTTAATACCAG AGACCCCCCCCCC] gap/C]TCCCCCTCC CCCTTCCCCCTCCC CCT	gap	C			SILENT- NONCODI NG	kinase	Human Gene SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.80E-173	
284	cg43917718	306	AGACGTGTCTGC CACAGGTCTCAG G/A/G]TAACAGAT GCCCTGTCCACT GAGAG	A	G			SILENT- NONCODI NG	kinase	Human Gene Similar to SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	1.40E-79	17
285	cg43928048	1876	TTTGATGGAAGG TTGTCCACACTG] G/A]GAATTATCAC ACACTTGATCAGG AA	G	A			SILENT- NONCODI NG	kinase	Human Gene Similar to SWISSPROT-ID:P20505 30 KD PROTEIN KINASE HOMOLOG (EC 2.7.1.-) (PROTEIN B1) - VACCINIA VIRUS (STRAIN COPENHAGEN), 300 aa.	5.30E-55	

286	cg42714751	208	CCCTCCGGATTG GGCGCGCGTGCG G[C/M]CCGCCGCG AGTGAGGGGTTTC GTGG	C	M				SILENT- NONCODI NG	kinaseinhibit or	Human Gene Similar to SWISSPROT-ID:P42771 CYCLIN- DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A) (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1) - HOMO SAPIENS (HUMAN), 156 aa.	2.60E-53	9 (9p21)
287	cg43322545	2943	TCCAAGCTAAGCA CTGCCACTGGGG A/GJAAACTCCACC TTCCCACTTTCCC AC	A	G				SILENT- NONCODI NG	kinaserecep tor	Human Gene SWISSNEW- ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)

288	cg43322545	3037	CCACCTCCATCCC AGACAGGTCCCTT C/GJCCCTTCTCTG TGCAGTAGCATCA CC	C	G			SILENT- NONCODI NG	kinaserecep tor	Human Gene SWISSNEW- ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcsl:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
289	cg43322545	3038	CACCTCCATCCCA GACAGGTCCCTCT C/GJCCCTTCTCTGT GCAGTAGCATCAC CT	C	G			SILENT- NONCODI NG	kinaserecep tor	Human Gene SWISSNEW- ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcsl:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
290	cg43980494	1040	GTCTGATAGAAGA GGAGCAGGAGAA A/GJCAAATCGTTA AAACCTAGCGAAT TC	A	G			SILENT- NONCODI NG	kinesin	Human Gene SPTREMBL- ID:Q14807 KID (KINESIN-LIKE DNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 665 aa.	0	16

291	cg43925424	374	TCAGGAGCAAGG CGAATGTATGACA [A/C]CATGTCCACA ATGGTGTACATAA AG	A	C				SILENT- NONCODI NG	kinesin	Human Gene SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	1.90E-304	14
292	cg42479188	305	TTCTGAAGAGGCT GACGATTTTACTJA /GJTCTCATTTTTT CCTTTCTCCAGAA	A	G				SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P13765 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DO BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 273 aa.	3.40E-147	6 (6p21.3)
293	cg42686658	1167	CTAGCTTCCCTTC CCATTCAACACA[A /C]ACACACATTCT TGCTCTACCCAAA G	A	C				SILENT- NONCODI NG	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
294	cg38337333	1122	TGCTCAAACCCA GCTTGCCAGCTC[T/C]AATGTACCAG CAGCTGGAATCTG AA	T	C				SILENT- NONCODI NG	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
295	cg27803682	2506	GTGGCTGGGCTA TTCCATCCATCTG[T/G]AAGCACATTT GAGCCTCCAGGC TTC	T	G				SILENT- NONCODI NG	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	3.50E-81	

296	cg21413267	1440	CGAGCGGCACCC AGAGCCTGCACC C/T/G/CCCTCACC GTCC/TCTGCGTC CCCC	T	G			SILENT- NONCODI NG	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	7.90E-79	
297	cg21413267	1860	AGGAGCCCTCTTC GGTGTCCTCCGAG T/C/GCCACGGTCA AGACCCGCAGCA CCA	T	C			SILENT- NONCODI NG	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	7.90E-79	
298	cg21413267	1890	CGGTCAAGACCC GCAGCACCAAAG C/A/G/CCGCCCCC GCACCTGCCCT GTCGC	A	G			SILENT- NONCODI NG	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	7.90E-79	
299	cg42481172	1541	GAGCCGTGTGGC TGTGGCCTCCGG G/A/C/GGCGGTGG ACGGCGTGCCT TCATC	A	C			SILENT- NONCODI NG	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.30E-71	1
300	cg39518465	89	GGGTGCACGGCC GGCCCTGGGCAG Ggap/CJGTAGCCA TGGAGCTGTGGC GCCAAT	gap	C			SILENT- NONCODI NG	oncogene	Human Gene SWISSPROT- ID:P15498 VAV PROTO- ONCOGENE - HOMO SAPIENS (HUMAN), 846 aa.	0	

301	cg41972699	627	ATGGGGCCGGTG TCTCGCCAGGAG G[ap]/C/GCAGACC CGGCTCCAGGGC CAGCGC	gap	C				SILENT- NONCODI NG	oncogene	Human Gene Similar to SWISSPROT-ID:Q64010 PROTO- ONCOGENE C-CRK (P38) (ADAPTER MOLECULE CRK) - MUS MUSCULUS (MOUSE), 304 aa.	2.40E-84	22 (22q11)
302	cg40333812	235	AGCATTGAGGAA GCATAACTGACG[C/T]GTGAAGGG GTGTGGGTACTT GCC	C	T				SILENT- NONCODI NG	oncogene	Human Gene Similar to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	1.40E-62	
303	cg43280482	2295	AGCATCTGCAGAC GACCCCGCAGC[A/C]TTTCCCTCGG ACCCCCCTCGAA GCC	A	C				SILENT- NONCODI NG	oncogene	Human Gene Similar to TREMBLNEW-ID:G2952331 ARG/ABL-INTERACTING PROTEIN ARGBP2A - HOMO SAPIENS (HUMAN), 666 aa.	3.90E-62	8
304	cg44014837	22	CACTGCTGTGCA GGGCAGGGA[A/T] GCTCCAGGCAGA CAGCCCGAGCAAA G	A	T				SILENT- NONCODI NG	oxidase	Human Gene SWISSNEW- ID:P08684 CYTOCHROME P450 3A4 (EC 1.14.14.1) (CYP11A4) (NIFEDIPINE OXIDASE) (NF-25) (P450-PCN1) - HOMO SAPIENS (HUMAN), 502 aa.lpcis:SWISSPROT-ID:P08684 CYTOCHROME P450 IIIA4 (EC 1.14.14.1) (NIFEDIPINE OXIDASE) (NF-25) (P450-PCN1) - HOMO SAPIENS (HUMAN), 502 aa.	8.00E-257	

305	cg41626506	3178	CAGCACAGCGAG CGCTCTCATTCTG [A/gap]CCCTTTTTC CTCTTCTCAGCCA ACT	A	gap			SILENT- NONCODI NG	peroxidase	Human Gene SWISSPROT- ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0	3 (3q26.3)
306	cg43918944	2958	TCTGTAGAGCTCT GAAAGGTTGAC] T/G]ATATAGAGGT CTTGTATGTTTTTA C	T	G			SILENT- NONCODI NG	phosphatase	Human Gene SPTREMBL- ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
307	cg43988365	1537	GACAGACGAGAC AGTGAGGTATGTG [A/G]GGCTGCTCC GGAATGGTCCGG AGGC	A	G			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT- ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5- PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa.[pcis:SPTREMBL- ID:Q14642 INOSITOL 1,4,5- TRIPHOSPHATE 5-PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.60E-227	
308	cg43969460	581	TAACTATGCAAGA CAAGACTTGGTCI C/G]TCACGTTCCG GTCTCTAGTTGAT TT	C	G			SILENT- NONCODI NG	phosphatase	Human Gene SWISSPROT- ID:P36876 PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55) - RATTUS NORVEGICUS (RAT), 447 aa.	1.90E-202	

309	cg43933809	362	AATTAAAACTCTA GGTGATACCTTAIT /CJATGGAAC TAGT TTATTCCTATTTA	T	C				SILENT- NONCODI NG	phosphatas e	Human Gene SWISSPROT- ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1- BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE), 327 aa.	1.60E-181	2 (2p23)
310	cg43931444	215	TGCTCGCGCCGT GCCACTAAGGTCA IC/TTCGCCGCCTC CGAGAGCCCCAGA GCCG	C	T				SILENT- NONCODI NG	phosphatas einhib	Human Gene Similar to SWISSPROT-ID:P39687 POTENT HEAT-STABLE PROTEIN PHOSPHATASE 2A INHIBITOR I1PP2A (HLA-DR ASSOCIATED PROTEIN I) (PHAPI) (ACIDIC NUCLEAR PHOSPHOPROTEIN PP32) (CEREBELLAR LEUCINE RICH ACIDIC NUCLEAR PROTEIN) - HOMO SAPIENS (HUMAN), 249 aa.	1.20E-89	9
311	cg42937321	1977	CTTTCCCTCTTA CCCTCTCTCTCTI G/TAAACATCGTAA ACAACAGACTTAC GT	G	T				SILENT- NONCODI NG	potassium_ channel	Human Gene SWISSPROT- ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)

312	cg42937321	1983	CCTCTTACCCTCT CTCTCTGAACATC /TJGTAAACAACAG ACTTACGTTAAAC T	C	T			SILENT- NONCODI NG	potassium_ channel	Human Gene SWISSPROT- ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
313	cg40991963	1357	CAAAATGTAACAG TGGCTTTTCAAC/A /GJGGAGTAAAGCA AAGTCTCTAAAGC T	A	G			SILENT- NONCODI NG	potassium_ channel	Human Gene SWISSPROT- ID:P48048 ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 1 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 1) (ATP-REGULATED POTASSIUM CHANNEL ROM-K) (KIR1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.80E-205	11 (11q24)

314	cg43951366	2332	AAAGATGTTTGAA TACTTAAACACTTG /AJTCACAAGATGG CAAAATGCTGAAA G	G	A				SILENT- NONCODI NG	prostaglandi n	Human Gene SWISSNEW- ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.lpcis:SP TREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0	1 (1q25.2)
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315	cg43951366	2829	TGGTGGAGCCAC TGCAGTGTATCT] T/C]AAAAATAAGAA TATTTTGGTTGAGA TA	T	C			SILENT- NONCODI NG	prostaglandi n	Human Gene SWISSNEW- ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.]pcis:SPTREMBL- ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN- ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0	1 (1q25.2)
316	cg43306254	1431	CACTTAACCTTGCA TGTCACACAGCTT] T/C]TGGTAACAAA TATCGCTAAACCT TA	T	C			SILENT- NONCODI NG	prostaglandi n	Human Gene SPTREMBL- ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)

317	cg43306254	1666	ATGTGATTAATTA TGTGATGAAAAC[A/T]TTTTTATAAA TGATCTTGGTCTA T	A	T			SILENT- NONCODI NG	prostaglandi n	Human Gene SPTREMBL- ID:O00325 PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM - HOMO SAPIENS (HUMAN), 402 aa.	1.40E-211	1 (1p31.2)
318	cg42918089	1064	CAATCAGAATTGA TAAGCACTGTTC[C/T]TCCACTCCAT TTAGCAATTATGT CA	C	T			SILENT- NONCODI NG	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE- 7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE- 7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.40E-146	11 (11q21)
319	cg44032168	1703	TCCATCCCTCTTT TGGGCTCTTCTG[G/C]AGGGAAGTAA CATTACTGAGCA CC	G	C			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT-ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.40E-82	2 (2q13)

320	cg43154190	1250	TACCCGGAAGTTG AGCTCAATTTCAIT /CJTCTGTTTTCT GGCCACAACCTGC CA	T	C			SILENT- NONCODI NG	protease	Human Gene Similar to SWISSPROT-ID:P50280 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE- 7) (MMP-7) (MATRIN) - RATTUS NORVEGICUS (RAT), 267 aa.	2.40E-59	11 (11q22)
321	cg43927549	175	CCCAGTCCTGCG GCTCCTACTGGG GIA/CJGTGCGCTG GTCGGAAGATTG CTGGA	A	C			SILENT- NONCODI NG	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
322	cg43927549	191	TACTGGGGAGTG CGCTGGTCGGAA Ggap/GjATTGCTG GACTCGCTGAAG AGAGAC	gap	G			SILENT- NONCODI NG	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)

323	cg43927549	52	CGGTCCGTGGTC CCCGGGGGCGCA Ggap/GJTCGCAGC GCTCCCGGCCCTC CAGGCG	gap	G			SILENT- NONCODI NG	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
324	cg43947066	780	TTCTCAAAAGGCT GGGGGTATTTAT A/GJTAAGAACTTA TTCCAAAGTGACT CT	A	G			SILENT- NONCODI NG	struct	Human Gene SWISSPROT- ID:O15142 ACTIN-LIKE PROTEIN 2 - HOMO SAPIENS (HUMAN), 394 aa.	3.30E-207	2
325	cg43923264	113	AGGAAAGCCGGA GAATTGGGGCAC G[C/gap]AAGAGGG GGGGCTTTGATG ACCCGC	C	gap			SILENT- NONCODI NG	struct	Human Gene SWISSPROT- ID:Q14012 CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I) - HOMO SAPIENS (HUMAN), 370 aa.	1.70E-200	3
326	cg43942332	1926	AGATTTCATCAGAA TAGGATTTTTCG[A /CJAAATCCCACCC ATATGCTGTTGAG C	A	C			SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.10E-124	11

327	cg43274705	580	CCGCTGTCTCTGT CTTCGCTTTTAA[G /TJTCAAGAAGAAAT AATGCGACGAAAA T	G	T				SILENT- NONCODI NG	struct	Human Gene Homologous to SPTREMBL-ID:Q28910 MUCIN - BOS TAURUS (BOVINE), 600 aa (fragment).	4.80E-110	12
328	cg42207316	146	CCACTTCTCTGGG ACACATTGCCCTT[C /TJTGTTTTCTCCA GCATGCGCTTGCT C	C	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSNEW- ID:P12273 PROLACTIN-INDUCIBLE PROTEIN PRECURSOR (SECRETORY ACTIN-BINDING PROTEIN) (SABP) (GROSS CYSTIC DISEASE FLUID PROTEIN 15) (GCDFP-15) (GP17) - HOMO SAPIENS (HUMAN), 146 aa. lpcds:SWISSPROT-ID:P12273 PROLACTIN-INDUCIBLE PROTEIN PRECURSOR (SECRETORY ACTIN-BINDING PROTEIN) (SABP) (GROSS CYSTIC DISEASE FLUID PROTEIN 15) (GCDFP-15) - HOMO SAPIENS (HUMAN), 146 aa.	3.50E-74	7 (7q32)
329	cg43927885	546	CATCATCATCATA GTTTACTTCAGC[A /TJCTTAAATCCCC GAGGAGTCTGCC CT	A	T				SILENT- NONCODI NG	struct	Human Gene Similar to SWISSPROT-ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.20E-55	17

330	cg40388639	5029	CTCTTGCCCAAGCC GGCTGCAAGTTT gap/TGTAAAGCGC GGGACAGACACT GCTGA	gap	T				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT- ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
331	cg43949316	555	AGGTTACCAACA GGAATACAAACACI C/TTCCTCCTCCCTT TTCTGCTCTAGAA GG	C	T				SILENT- NONCODI NG	synthase	Human Gene SWISSPROT- ID:P48651 PHOSPHATIDYL-SERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) (EC 2.7.8.-) (KIAA0024) - HOMO SAPIENS (HUMAN), 473 aa.	9.80E-269	8
332	cg43958714	1565	TGGGTGATGATCA CTGTGCTGCTTG T/CJGGCTCATGGC AGAGCATTGAGTG CC	T	C				SILENT- NONCODI NG	synthase	Human Gene Similar to SPTREMBL- ID:Q42761 SQUALENE SYNTHASE (EC 2.5.1.21) (FARNESYL- DIPHOSPHATE FARNESYLTRANSFERASE) (FARNESYLTRANSFERASE) (PRESQUALENE-DI- DIPHOSPHATE SYNTHASE) - GLYCERYLHIZA GLABRA, 412 aa.	9.20E-83	8

333	cg43275028	2508	ACAGACTGGCTG CAGCATTAGGAAT [C/T]AGGTCATTCC GAAACTCATCAT GA	C	T			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
334	cg43275028	2535	GGTCATTCGGAAT CTCATCATTTGAA[T /C]CAGGAAGAAGA AGAGTTCAATCTT A	T	C			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

335	cg43275028	2601	AGAATGGCACTGA ATTGTTTCTTCIA/ GJACACAGATAT AATTGTTGGTTCA A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcds:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
336	cg43275028	2873	CTTTCACCTTGGTG CTGGAGAATTCAI A/GJAAGTCAAGAA CATGCTAAGCATA AG	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcds:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

337	cg43275028	2894	TTCAAAAAGTCAAG AACATGCTAAGC A/GJTAAGGGACCC AAGGTAGAAAGA GAT	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
338	cg43275028	3073	TTCTCCTTCCAGA ATGAGGCCCTGG A/GJAGGACCCCTCC TAGTGATCTGTTA CT	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcis:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)

339	cg43275028	5590	ACTACATAAGGAC AGCAACATGCCTI A/GJTGACATGAG AGAAATTTGTCTTA CT	A	G			SILENT- NONCODI NG	synthase	Human Gene Similar to SWISSPROT-ID:P70490 MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (O- ACETYL GD3 GANGLIOSIDE SYNTHASE) (AGS) (MFGM) - RATTUS NORVEGICUS (RAT), 427 aa.lpcIs:SPTREMBL-ID:P70490 O- ACETYL GD3 GANGLIOSIDE SYNTHASE - RATTUS NORVEGICUS (RAT), 427 aa.	3.20E-65	1 (1q23)
340	cg43985000	1856	GAAGAAAAATCACA AGGCAACTGTGA C/GJTCCGGGAATC TCCTCTCTGATCC TT	C	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P25101 ENDOTHELIN-1 RECEPTOR PRECURSOR (ET-A) - HOMO SAPIENS (HUMAN), 427 aa.	1.60E-236	4
341	cg39565524	1684	TCCGACCCCCACA CACCCCTGAGGGA G/C/GJCCCTACCCT AGCCTCAGCCGC TCCTG	C	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P51575 P2X PURINOCEPTOR 1 (ATP RECEPTOR) (P2X1) (PURINERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 399 aa.	2.00E-220	17
342	cg43306266	1603	ATAATCCATGCCT CTGAATATTAGAT /GJTGTTTCTTGG ATGGGATTTTGAA T	T	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

343	cg43306266	1641	GGGATTTTGAATA TGCATTTAAGAA[G ap/C]GTTGGGAAG AATTCACAGATG ATG	gap	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)
344	cg43306266	1650	GAATATGCATTTA AGAAAGTTGGGAA[G/C]AATTCACAG ATGATGATTGGAG GA	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.80E-212	1 (1p31.2)

345	cg43329467	683	TCGGCAAATCTTG AAAGCTGCAGGG[C/T]GCAGAGACAT GGATGTGACTTCC CA	C	T			SILENT- NONCODI NG	tm7	Human Gene SWISSNEW- ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW- INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) (GPCR-BR) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:SWISSPROT-ID:Q99527 CHEMOKINE RECEPTOR-LIKE 2 (IL8-RELATED RECEPTOR DRY12) (FLOW-INDUCED ENDOTHELIAL G PROTEIN-COUPLED RECEPTOR) (FEG-1) (G PROTEIN-COUPLED RECEPTOR GPR30) - HOMO SAPIENS (HUMAN), 375 aa.lpcis:TREMBLNEW-ID:G2656121 G-PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 375 aa.	8.20E-201	7
346	cg2751286	439	AAGGCATAAGAAC TAGGAGCTGCTG[gap/GIACATTTCAA TATGAAGGGCAAC TCC	gap	G			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P50052 TYPE-2 ANGIOTENSIN II RECEPTOR (AT2) - HOMO SAPIENS (HUMAN), 363 aa.	2.00E-197	X

347	cg11751407	76	GAATGTGGGGAT AAGGCATTGGGA C/C/TCTATCAGGT ATCCTGAGGAGA GACT	C	T			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P46089 PROBABLE G PROTEIN- COUPLED RECEPTOR GPR3 (ACCA ORPHAN RECEPTOR) - HOMO SAPIENS (HUMAN), 330 aa.	3.20E-176	1
348	cg43326635	135	CAGCCGGGAGCT CTGCCAGCTTTGG [C/T]GAAGGAGGG TGCTTGCCCTCGTG CCC	C	T			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
349	cg43326635	139	CGGAGCTCTGC CAGCTTTGCCGAA [G/C]GAGGGTGCT TGCCCTCGTGCCC CTTG	G	C			SILENT- NONCODI NG	tm7	Human Gene SWISSPROT- ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
350	cg43993798	1839	TGCTCTTGCTGCT GATGGAGGAGGA A/G]GGGGTGGAT CCCGTGGAGCCT CCAA	A	G			SILENT- NONCODI NG	tm7	Human Gene Homologous to SWISSPROT-ID:P31421 METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR - RATTUS NORVEGICUS (RAT), 872 aa.	6.90E-109	3

351	cg43040271	2130	ATGCTTCCCCCAA CCCTAGGGAATC[A/C]ACACTTAAGA TAAATCGCCACTT CT	A	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.lpcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	
352	cg43040271	2139	CCAACCCCTAGGG AATCAACACTTAA[G/T]ATAATTCGCC ACTTCTCCTCTTT CT	G	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.lpcds:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	

353	cg43040271	2163	AGATAATTGCGCA CTTCTCCTCTTT[C /TTCTCTGCTCCG CTCACGGCTTGCA G	C	T			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.pcls:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.90E-74	
354	cg43040273	1668	CGCAGAGCCCCG CCGTGGGTCCGC CTT/CJGCTGAGGC GCCCCCAGCCAG TGCGC	T	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
355	cg43040273	1760	CAGCGCCTTCTTG CTGGCACCCAAT A/GJGAAGCCATGC GCCGGACCCACGA CGT	A	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
356	cg43040273	1793	TGCGCCGGACCA CGACGTCACGCA G/C/GJAAAGGGAC GAGGTGTGGGTG GTGGG	C	G			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)

357	cg43040273	2767	GCAGGTCCTCTTT GAAGGCCTATGG[G/C]AATGGCTACT CCAGCAACGGCA ACA	G	C			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
358	cg43040273	2953	ATTGTAGTACAAA TGACTCACTGCT[G/A]TAAAGCAGTT TTTCTACTTTTAA G	G	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
359	cg43040273	3053	ATAAACTTAGAAT AAAAATTGTAAA[ap/A]TTGTATAGAG ATATGCAGAAAGGA AG	gap	A			SILENT- NONCODI NG	tm7	Human Gene Similar to SWISSPROT-ID:Q24563 DOPAMINE RECEPTOR 2 - DROSOPHILA MELANOGASTER (FRUIT FLY), 539 aa.	2.00E-58	5 (5q32)
360	cg43998970	1501	AGGGTGGAAC GCTGATGGGATTT [gap/T]CCTTCATTC CCTTCTGATAAAG GTA	gap	T			SILENT- NONCODI NG	transcriptfac tor	Human Gene SPTREMBL- ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
361	cg43998970	249	AGCCTCCCCAGA GACAACACCGGG A[G/C]CCTCATCTC TCTCCTCACCCCTG CTG	G	C			SILENT- NONCODI NG	transcriptfac tor	Human Gene SPTREMBL- ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12

362	cg43947199	2623	GTCTTCTCCGGC CCACCCCGCTGG C/TAAAGGGAGT GGCGAAGCTGG AGC	C	T			SILENT- NONCODI NG	transcriptfac tor	Human Gene SWISSNEW- ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.lpcis:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.20E-158	8
363	cg43917396	934	GGGGCCGGGCAC TGCCAGGAAGG G/A/G]CTCCGGGA GAGGAGCCGGC GGCTG	A	G			SILENT- NONCODI NG	transcriptfac tor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
364	cg40351913	2030	AGACGAAGACCC CAGGAAGTCATCC [T/C]GCAATGGGA GAGACACGAACA AACC	T	C			SILENT- NONCODI NG	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
365	cg43921289	237	CCCACGCCTGCC AGGAGCAAGCCG A[gap/A]GAGCCAG CCGGCCGGCGCA CTCCGA	gap	A			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1

366	cg43928515	3196	AAACAAATAAGCC CTTTTACTGAC[A /G]ATGCACCCAAC CTTTTCAGCTGAA G	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
367	cg43955093	1309	AGAGTCAAAAATC CAAGTTTGGATT[C /G]TAAGCAGCCTT GACAGTAATCACT G	C	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
368	cg43955093	1336	AAGCAGCCTTGAC AGTAATCACTGA[A /G]TGGTAGGGAAA AAAAGACAGTTGG G	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
369	cg43925474	2206	AGGCAAAAAGCTCA CAGTAAATGTAT[A /C]CCAGAACAGG GGCCTAAGTGAA GGT	A	C			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P42566 EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN) - Homo sapiens (Human), 896 aa.	0	17
370	cg44014437	4893	CTGCTCCCANCTT CGCCAGCCTCCA[A/G]TGTAACAATT CCGCGTGTAGTG GGC	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P53675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0	17 (17q11)

371	cg44014448	5114	CTGCTCCCAACTT CGCCAGCCTCCA[A/G]GTACAACTT CCGCGTGTAGTG GGC	A	G				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P53675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0	17 (17q11)
372	cg43973129	2242	CACTTCACTGAAA GACACCATTTAT[C /A]TACCCAAGGGC AGAAAAGTAGAACT T	C	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P05060 SECRETORANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)
373	cg43950657	1939	GATAGGACTCAAG CTTATTGGGAT[C /T]CTGATCAATTC TTTCTGATGTTGT T	C	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0	21 (21q22.1)
374	cg43956384	2416	TACAGCCATCTGT ACCTACTGGAGC[C/T]GCAGAAAGG AAGTCCACTCAGT CAC	C	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P13866 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 664 aa.	0	22 (22q13.1)

375	cg43992229	101	AGCAGTGCAGCC CCGGCGCGGAGC A[G/A]GGAGCCTC GGCCCGCGCCCG GCGCC	G	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
376	cg44932392	260	GAGAAAAAGCATG GTACCCAACCGA[A/T]TTTCCACTTTT CAGCAATACTTCA C	A	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
377	cg44932392	323	TAAAGTTTAAAGA AATGTCATAATG[A /T]CATGAGCTTGA AATATCTCTAGGC A	A	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
378	cg43981656	1121	AGCAAAGAAACAC TGGCAGAATTCC[A/T]GCATTGCAA AATTCTAAGTTTT GG	A	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.60E-292	10
379	cg44910613	366	AAATAAATGTTTT CATAGTCATTAC[T /A]CTTTACAATGG GAGTGCTAAATT C	T	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P38567 HYALURONIDASE PRECURSOR (EC 3.2.1.35) (SPERM SURFACE PROTEIN PH- 20) (SPERM ADHESION MOLECULE 1) - Homo sapiens (Human), 509 aa.	1.20E-280	7

380	cg44035104	189	AACTGGGTTGCTC TAAGAACTGATG(T /C)CTAAACCGTCT CAGCATGGCCTG TA	T	C				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P37287 N- ACETYLGLUCOSAMINYL- PHOSPHATIDYLOSITOL BIOSYNTHETIC PROTEIN (GLCNAC-PI SYNTHESIS PROTEIN) (PHOSPHATIDYLOSITOL GLYCAN COMPLEMENTATION CLASS A) (PIG-A) - Homo sapiens (Human), 484 aa.	4.70E-261	X (Xp22.1)
381	cg43929959	1643	CAATGCATGAATC TGTAACCTTCGG[G/gap]AGGGCACT CACATGCCGCCCC CCAGC	G	gap				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SPTREMBL- ACC:P78506 DIABETES MELLITUS TYPE I AUTOANTIGEN (ISLET CELL AUTOANTIGEN P69) - HOMO SAPIENS (HUMAN), 483 aa.	2.10E-258	7
382	cg43950250	1961	TGTTTCATGATTT CTTGATGTTCTTC[/gap]TAATGGAAAA CTAAGAGATGGAA TT	C	gap				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P11926 ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC) - Homo sapiens (Human), 461 aa.	7.00E-251	2
383	cg43064090	129	GCCGAGTCCGCT GGTGGCGGACC CIA/TAGGGGAGC AGCCAGTAGGGA AGTTG	A	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P32754 4- HYDROXYPHENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (HPD) - Homo sapiens (Human), 392 aa.	4.80E-213	

384	cg43064090	130	CCGAGTCCGCTG GTGGCGGACCC AIA/TJGGGAGCA GCCAGTAGGGAA GTTGG	A	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P32754 4- HYDROXYPHENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (HPD) - Homo sapiens (Human), 392 aa.	4.80E-213	
385	cg43064090	157	GGGAGCAGCCAG TAGGGAAGTTGG G[C/G]GAGTTCCA GAATCAGGGGGC GTGGC	C	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P32754 4- HYDROXYPHENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (HPD) - Homo sapiens (Human), 392 aa.	4.80E-213	
386	cg43064090	61	TAATCGGGAGGG CTGGAGCAGAGG G[C/G]GGCCCCGC CGAGGGGCGTGG TCAGT	C	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P32754 4- HYDROXYPHENYLPYRUVATE DIOXYGENASE (EC 1.13.11.27) (4HPPD) (HPD) - Homo sapiens (Human), 392 aa.	4.80E-213	
387	cg30490224	3296	GATGCCAAAAAAA CAAAGGTGAGAA A/C[CCACAACACA GGTCTAAACTCAG CA	A	C			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P30968 GONADOTROPIN- RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.20E-177 4 (4q21.2)	
388	cg43924431	381	GTCTTTTACAGAT GGTTTTTCAAAA /gapJAGAGTCCAG TAAATATTTTCAC ATT	T	gap			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.20E-166 5	

389	cg43936047	607	CGTTGTTCTCTAAT GTGGATCTACCA[C/T]CCCCTGTGTC ATCGAGATTCGG TC	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene TREMBLNEW- ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.30E-164	13
390	cg43272443	1542	TGGGATTACAGGT GGCAGCTACCA[A/G]CCCAAGCTAAT TTTTGTATTTTGA G	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SWISSNEW- ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.70E-158	1 (1p22)
391	cg43966848	2065	CCTTCAGCACCCCC TGCAGCGGAAA[C/T]AATGAGCCGC CGTAGCCGCCCAT CCG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q92600 PROTEIN INVOLVED IN SEXUAL DEVELOPMENT, COMPLETE CDS - HOMO SAPIENS (HUMAN), 299 aa.	4.90E-156	2
392	cg43964140	176	AAAAAGCTACAGA AAAGAAATCACT[T /C]TGAAAAACACA ATGACTCAGAGG CA	T	C			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to TREMBLNEW-ACC:AAC69899 SACM21 - MUS MUSCULUS (MOUSE), 721 aa.	1.10E-150	6
393	cg43285114	418	CAGGGACATGCG GGCACCCCGTGG G[G/gap]TCTTTGG CGGCTCACAGGA CAATGG	G	gap			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to TREMBLNEW-ACC:AAD23440 LR8 - HOMO SAPIENS (HUMAN), 270 aa.	1.90E-138	7

394	cg43948566	370	GCAGGCAGAGCA CCCTGGGACCCC A[G/gap]GGCAGAA GGACCCCTGCC TCCAGT	G	gap			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene H SWISSNEW-AC :P18582 CD81 ANTIGEN (26 KI CELL SURFACE PROTEIN TAPA 1) - Homo sapiens (Human), 236 aa	3.30E-125	11
395	cg44003626	649	TAAACAGCTCAGT TCAGGGACTGGT A/G]TACAAAGCTGG CCACCCATCTCAG CC	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene H SPTREMBL-AC :Q15025 MRNA (HA1652) FOR JRF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.70E-123	
396	cg43917206	259	TTACAGGACATCA CCTGCCATCTTAT /A]GGTTTAATATT ACAAATGCCTAGT	T	A			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene H SWISSPROT-CC:P22061 PROTEIN-L-ISOASPARTATE(D- ASPARTATE) - METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN L-ISOASPARTATE - HOMO SAPIENS (HUMAN), 226 aa	6.90E-118	6

397	cg43289666	215	GGCCGATTTTCC ACAAATTTAAATC[C] TTCAGTTCACCTG GTATCCAGCTCCA G	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to SPTREMBL-ACC:O00559 CANCER ASSOCIATED SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 213 aa.	2.50E-111	8
398	cg43986282	840	GTTTCCACCTCCC CAGACAGGCATT[C/TTCGAGTGGGA GGCGGGAGCACG TACC	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
399	cg43986282	841	TTTCCACCTCCCC AGACAGGCATT[C] C/TJGAGTGGGAG GC GGGAGCACGT ACCG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
400	cg43297716	1030	CTAAACCCCAAATG GGGGCTGCTGGC[A/TJGACCCCGAG GGTGCCTGGCCA GTCC	A	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION-STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa.	1.20E-106	22 (22)

CG43980312

401	cg43980312	2160	TTTTATCATTAAAG TGCCAGAAATGG[C/ T]TCTTTAATGAAA ACAAAAAACAAAG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.90E-101	8 (8q22)
402	cg43939240	624	GGAGGGTTGGAG TCACTGACGAATG [C/T]GAGCCGGGC CAGGCCCATGCA AAG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SP TREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1.00E-100	
403	cg43941552	881	GCCACCTGCCCG GGCTGTGGAGGA G[C/gap]GCTCGCG CTGACCAGGCGC TGGGGC	C	gap			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.60E-100	
404	cg43941552	1124	GCTTCTGCCCA CCGCAGGGACAA A/G]CCCTGGAGAA ATGGGAGCNTGG GGA	A	G			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.60E-100	

405	cg42917153	914	CATTCTCTTTGT ACATAATACATTIC /TACCTCCCTGCC TCCTCTCCTTTCT A	C	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P45973 HETEROCHROMATIN PROTEIN 1 HOMOLOG ALPHA (HP1 ALPHA) (ANTIGEN P25) - Homo sapiens (Human), 191 aa.	2.10E-100	12
406	cg43927693	878	CAGGGGTCAGCA GAGCTTCAGAGG TIG/TGCCCCCACC TGAGCCCCCACC CGGGA	G	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.30E-95	22
407	cg43951338	507	CAGAAAGCAGCA AATTAGTGTTTTT C/AJAGGACCGAAT TCGGCTCCCGCA GCT	C	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P36405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10
408	cg43951338	511	AAGCAGCAAAATTA GTGTTTTTTCAGGIA /CJCCGAAATTCGGC TCCCGCAGCTCCT G	A	C				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P36405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10
409	cg43951338	547	CTCCCGCAGCTC CTGCATCTCCATTI C/TGTCTAGATT TATTCTCTCTTTGC A	C	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P36405 ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.40E-93	10

CG25236776

410	cg25236776	1234	CCGCCCCAGCCC GACGCCCTACTGA G[gap]/TCCCCGCG CTCGCCCCACCG GCGCGC	gap	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	
411	cg25236776	1240	CCAGCCCGACGC CTACTGAGCCCC G[C]/TGTCTCGCCC CACGGCGCGCT CTTCG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	
412	cg25236776	1242	AGCCCGACGCCT ACTGAGCCCCGC G[C]/TTCGCCCA CCGGCGCGCTCT TCGCG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	
413	cg25236776	1246	CGACGCCTACTG AGCCCCGCGCTC G[C]/TCCCCACCGG CGCGCTCTTCGC GCCCG	C	T			SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	

cg43968406 1362 GCTACGTTTACTC
ACAGCCAGCGAA
gap/A]CTGACATTA
AAATAACTAACA
ACA

414	cg43968406	1362	GCTACGTTTACTC ACAGCCAGCGAA gap/A]CTGACATTA AAATAACTAACA ACA	gap	A						Human Gene Similar to REMTREMBL-ACC:E47283 DNA FOR ORF1 AND ORF2 FROM CHROMOSOME X - HOMO SAPIENS (HUMAN), 157 aa.	5.00E-83	X (Xp11.4)
415	cg42748886	104	CGCCTCTGATCCA AGCCACCTCCCGI C/T]CAGAGAGGTG TCATGGGCTTCCA AA	C	T						Human Gene Similar to ACC:P01258 CALCITONIN PRECURSOR - Homo sapiens (Human), 141 aa.	2.00E-70	11 (11p15.2)
416	cg43969533	356	CTCTGCACAAGG GAAGCCTATCCTA T/gap]TTTTTTTT CCTTTGCGAAAC AGA	T	gap						Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.60E-67	7
417	cg43976681	1119	AATGCCCTCAGATC AGTGACCCCAAGG A/gap]ACCTTCCAG AATGGATGAAATA GAC	A	gap						Human Gene Similar to TREMBLNEW-ACC:AAD29427 MYOMEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.	4.30E-66	11
418	cg43976681	1120	ATGCCCTCAGATCA GTGACCCCAAGG A/gap]CCTTCCAGA ATGGATGAAATAG ACC	A	gap						Human Gene Similar to TREMBLNEW-ACC:AAD29427 MYOMEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.	4.30E-66	11

CG43984044

419	cg43984044	714	CCAAGCGGAAGG CCATTTCCCTGC[C/TCTTCTCTCAGT TGTCGGGGGCGG GGG	C	T				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.30E-66	19
420	cg43933283	398	CTAATTGTGTCGA ATTTCAGGATT[G /A]GAGGAAAAGTT GCTCCCTTTTCAGC C	G	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P05062 FRUCTOSE-BISPHOSPHATE ALDOLASE B (EC 4.1.2.13) (LIVER- TYPE ALDOLASE) - Homo sapiens (Human), 363 aa.	6.60E-65	9 (9q22)
421	cg42381630	577	AAAGCAATCACAG TGTTAAAGAAAG[G/A]CACGTTGAAA TGATGCAGGCTG CTC	G	A				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
422	cg41664708	423	CCAGCCAGCTCAT TTCACTTTACAC[G /C]CTCATGGACTG AGTTTATACTCAC C	G	C				SILENT- NONCODI NG	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2.00E-54	1

Genetic

423	cg43277632	3906	AGCCTTCCCGCA GAAAAAGATGCAG [C/T]CCCCCAGAC CTTCTCTGTGCTG ATT	C	T	Ala	Val (652)	CONSER VATIVE	ATPase_as sociated	Human Gene SWISSPROT- ID:P35670 COPPER- TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
424	cg40310734	1138	TACCAGAGGCTG CATCGGCTGCGC G[C/G]AGAGCAGA TGGCGTCGTATTT TGGG	C	G	Ala	Gly (653)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
425	cg40310734	1238	TGGTGGGCGCTC CACTGTATATGGA [G/C]AGCCGGGCA GACCGAAACTG GCCC	G	C	Glu	Asp (654)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
426	cg40310734	1893	CTCTCAACAGGCA GGCACCACCCCTG A/GJACCTGGATCT GGGCGGAAAGCA CAG	A	G	Asn	Asp (655)	CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)

427	cg43982507	1883	GGTACAAGTGTG AATGTAGTCGTG G/CJCTATCAAATG GATCTTGCTACTG GC	G	C	Gly	Ala (656)	CONSER VATIVE	eph	Human Gene SWISSPROT- ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
428	cg41554010	949	GCCGAGGACGTG CGTGGCAACCTG A/G/AJGGGCAACA CCGAGGGGCTGC AGAAG	G	A	Arg	Lys (657)	CONSER VATIVE	eph	Human Gene SWISSNEW- ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.jpclis:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203	11 (11q23)
429	cg43299024	1036	TACGAGGTGCCC TTGGAGACCCCG C/A/GJTGTCACAC GCCGGGCACCGT CCCCA	A	G	His	Arg (658)	CONSER VATIVE	glucoamylas e	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)
430	cg43299024	1108	GAGGAGCCCTTC GGGGTGATCGTG C/A/GJCCGGCAGC TGGACGGCCGCG TGCTG	A	G	His	Arg (659)	CONSER VATIVE	glucoamylas e	Human Gene TREMBLNEW- ID:G2826521 MALTASE- GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

431	cg43285373	12840	GACTGACTGGGG AAAGGAACCTAAA [A/C]TCGAGTCTG CCTGGATGAATG GAGA	A	C	Ile	Leu (660)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT- ID:P98164 LOW-DENSITY LIPOPROTEIN RECEPTOR- RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) - HOMO SAPIENS (HUMAN), 1751 aa (fragment).	0	2
432	cg36834323	1004	AGTTATTCTAGAG GATACAGAAATC[A/G]TCGAAAGTTCC CGAGAAACTAGG GAG	A	G	His	Arg (661)	CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
433	cg41568631	2101	GGACCAGGGGGC CATGCTGCTCAAT [G/A]TCTCAGGCC ACGTCAAGGAGA GCGG	G	A	Val	Ile (662)	CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
434	cg42359655	666	TGCTTTTCAGGGC GGAAAACTCTCT[A/G]TTGTCTCGCG AGCTGAAGATATC CC	A	G	Ile	Val (663)	CONSER VATIVE	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYL CERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)

435	cg43998672	1331	GTGTGGGCCTTG GTGAACCTCTAGCA [C/A]GCCGGCTAAT GTCTCCTGGTTTG GTC	A	Val	Leu (664)	CONSER VATIVE	hydroxyster oid	Human Gene SPTREMBL- ID:Q13194 11-BETA- HYDROXYSTEROID DEHYDROGENASE TYPE 2 - HOMO SAPIENS (HUMAN), 405 aa.	2.00E-220	16 (16q22)
436	cg43969028	1133	GGAGATGTGGTC ATTCCTAGTGATT A/T]TTTTCAGATA GTGGGAGGAAGC AAC	T	Tyr	Phe (665)	CONSER VATIVE	immunoglob	Human Gene Homologous to SPTREMBL-ID:P91456 SIMILAR TO THE IMMUNOGLOBULIN SUPERFAMILY - CAENORHABDITIS ELEGANS, 1173 aa.	2.20E-149	18 (18q21.3)

437	cg43933479	133	AAGGAGAAGAGA AAGCTGTTTATCC[A/GJTTCATGGGT GAAGGTACAATAA AT	A	G	His	Arg (666)	CONSER VATIVE	interleukin	Human Gene SWISSNEW- ID:P29466 INTERLEUKIN-1 BETA CONVERTASE PRECURSOR (IL- 1BC) (EC 3.4.22.36) (IL-1 BETA CONVERTING ENZYME) (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) (CASP-1) - HOMO SAPIENS (HUMAN), 404 aa.lpcds:SWISSPROT-ID:P29466 INTERLEUKIN-1 BETA CONVERTASE PRECURSOR (IL- 1BC) (EC 3.4.22.36) (IL-1 BETA CONVERTING ENZYME) (ICE) (INTERLEUKIN-1 BETA CONVERTING ENZYME) (P45) (CASPASE-1) (CASP-1) - HOMO SAPIENS (HUMAN), 404 aa.	2.50E-206	0	10
438	cg43942537	1163	GCCACTGTCTCTT CCAAACCCCTTCA[C/A]GCCTTGCTT GCTTGTCTCGTC TA	C	A	Val	Leu (667)	CONSER VATIVE	kinesin	Human Gene SWISSNEW- ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.lpcds:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.			

439	cg38337333	1035	TTCCAAATGCTGA GCCCAGAGCGTTI G/AJTCTCCTGCC ATGAGCACCCACA GTC	G	A	Val	Ile (668)	CONSER VATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
440	cg38337333	271	CTGGAACAGTTTC CTCATTAGCCCTI G/CJTGACCCAG CACACGCAGGGA CCTA	G	C	Val	Leu (669)	CONSER VATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
441	cg38337333	823	TCATCGCTGGTGC TCCAAAAAAA/A /GJATGCTGCTGTA ATGAACCAAGAGC C	A	G	Asn	Asp (670)	CONSER VATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
442	cg30421838	3434	GGATGCTGTTGCT CTCCACAGCCAI G/TJGGCGTTCC AAATGAAAGCCAA GC	G	T	Val	Leu (671)	CONSER VATIVE	nucI_recept	Human Gene SWISSNEW- ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. JcIs:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (1)

443	cg43064060	1019	GCCAAATGGCATC CAGAACCAAGGAG G[C/T]GGAGGTCC GCATCTTTCACTG CTGC	C	T	Ala	Val (672)	CONSER VATIVE	nucl_recpt	Human Gene SWISSPROT- ID:Q07869 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA) - HOMO SAPIENS (HUMAN), 468 aa.lpcis:SPTREMBL-ID:Q16241 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA - HOMO SAPIENS (HUMAN), 468 aa (fragment).	4.10E-254	22
444	cg43991813	1860	TCTCGACTAACAG CATTCCAAAGA[T /C]GGAGCGAATAT TGTCACACGGTTGA G	T	C	Ile	Val (673)	CONSER VATIVE	nuclease	Human Gene SWISSPROT- ID:P40692 MUTL PROTEIN HOMOLOG 1 (DNA MISMATCH REPAIR PROTEIN MLH1) - HOMO SAPIENS (HUMAN), 756 aa.	0	3 (3p21.3)
445	cg42904626	194	GAGTGCCTTGAC GATACAGCTAATTJ C/GJAGAAATCATTT TGTGGACGAATAT GA	C	G	Gln	Glu (674)	CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:P01118 TRANSFORMING PROTEIN P21/K- RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
446	cg42904626	548	AAGAAGTTATGGA ATTCCTTTTATT[G/ C]AAACATCAGCA AAGACAAGACAG GG	G	C	Glu	Gln (675)	CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:P01118 TRANSFORMING PROTEIN P21/K- RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12

447	cg42460457	2845	GCCGCCCTCAGCC AGCAAGCAGGCG G[C/T]TAGGCCAG TCCTAGCCACCCAC AGAG	C	T	Ala	Val (676)	CONSER VATIVE	phosphate	Human Gene SWISSPROT- ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R-PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
448	cg43272594	582	GGGATGTAAGTGC ATGGTGTTCTTGG [T/C]GCTGTATGTG CAGGCACGACTC TGT	T	C	Val	Ala (677)	CONSER VATIVE	phosphate	Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.40E-79	19
449	cg43958858	807	TCAGGTGGTGGG AACCTACCGTTGC [C/G]TTCCTGGAA AGAAGGGAGGCT ACAC	C	G	Leu	Val (678)	CONSER VATIVE	polymerase	Human Gene SWISSNEW- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa. pcls: SWISSPROT-ID: P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)

450	cg43916732	540	GTACAGCGGGCG GGCCACCTCGG C/A/TCTGAGCAC CAATTTTGGGGG GGCG	A	T	Thr	Ser (679)	CONSER VATIVE	protease	Human Gene SPTREMBL- ID:Q15113 PROCOLLAGEN C- PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.20E-247	7 (7q21.3)
451	cg42894809	2745	GGATGCTGGAGA GTGGATCACTGTC [A/G]ATCAGACGA CAACAGCCAACC GTTA	A	G	Asn	Asp (680)	CONSER VATIVE	struct	Human Gene SWISSPROT- ID:P54296 M-PROTEIN (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN- ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	8
452	cg40388639	2337	GATTCCTCCAGAG CTGGTGTGGAA[G/C]TTCCCATCAG GCACCCCAAGTTT GA	G	C	Val	Leu (681)	CONSER VATIVE	synthase	Human Gene SWISSPROT- ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
453	cg40388639	2380	AAGTTTGAGTGGT TCAAGGACCTGG[G/C]GCTGAAGTG GTACGGCCTCCC CGCC	G	C	Gly	Ala (682)	CONSER VATIVE	synthase	Human Gene SWISSPROT- ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)

454	cg43124627	1524	AATTTCTATATCA CTGGGGACAGAG[C/G]ATATATGGAT AAAGATGGGTATT TC	C	G	Ala	Gly (683)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16
455	cg43124627	869	TGGAACAAGTGG ATATCCGAAAATG[A/T]CTGCACACAC CCACAGCAGTTTT GG	A	T	Thr	Ser (684)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.lpcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.70E-79	16

456	cg43064068	1464	AGGAGAGGTGGT GAAGGCATTGTG [G/A]TCCTGGCCT CGCAGTTCCTGTC CCA	G	A	Val	Ile (685)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
457	cg2514276	1090	GTGATGGACCCT CTCATATATGCCT[A/T]CCGCAGCCAA GAGATGCCGGAAG ACC	A	T	Tyr	Phe (686)	CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5-R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa.	7.00E-172	
458	cg32423505	964	TTCCATCTGAGGT TTATAAACCCACG[A /T]ATTTCAGGCCAA GTGGCCAGGAATG GC	A	T	Phe	Tyr (687)	CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.20E-55	3 (3q21)
459	cg43335558	344	CAAGACCTAGCTC CCCAGCAGAGAG[C/T]GGCCCCACAA CAAAAGAGGTCCA GC	C	T	Ala	Val (688)	CONSER VATIVE	tnfreceptor	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8

460	cg43998970	1347	GACAGAGCTGTA CCGTGACATTTTC[C/GJAGCACCTTCG GGATGAATCAGG CAA	C	G	Gln	Glu (689)	CONSER VATIVE	transcriptfac tor	Human Gene SPTREMBL- ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12
461	cg2537639	800	GAGGGCGATTCT ACTACCTGGGG[G/CJGTTCTTCGGG GGTCGGTGCAA GAG	G	C	Gly	Ala (690)	CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYLTRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)

462	cg43935995	1552	AGTGTCCTCACC ATGGTCACCCCTG[A/G]TCACCCCTGCC TCTGCTTTTCCTT CT	A	G	Ile	Val (691)	CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q03518 ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 1) - HOMO SAPIENS (HUMAN), 748 aa.	0	6
463	cg43935986	1424	CCTGGAACGCGC CTGTACCTGCTC [G/A]TAAGGAGGG TGCTGCACCTTGG GGGT	G	A	Val	Ile (692)	CONSER VATIVE	transport	Human Gene SPTREMBL- ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0	6 (6p21.3)
464	cg43968274	730	GAGCACGAGGAA GCCATGAATGCG G[C/T]CTACTCAG GCTACGTCTACAC GCAC	C	T	Ala	Val (693)	CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:O14914 NEURONAL MUNC18- 1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
465	cg44018598	3568	AGATACTTTCTAT AAGCAGTTTTTTA[G /C]ATTGTAGGAAG CAGCTGAATTCAA A	G	C	Leu	Val (694)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14

466	cg44926796	1825	ACACTGGAAAGCA CAACAGTTGGCA C/GTTCTGCTAG AAATAATAATTG CA	C	G	Thr	Ser (695)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:Q15046 LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS) (KIAA0070) - Homo sapiens (Human), 597 aa.	0	16
467	cg43055918	1622	AACGCTGCCCTG ACTGAGAAAGGC A/C/T/GATGCTCG CTCCACTGCTGGA ACCG	C	T	Arg	His (696)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
468	cg43966985	1381	CATCCAGGACAAC TTCTCGGTGACTT C/G]AAGTGCCCTT CACTGAGAGCGC CTG	C	G	Gln	Glu (697)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P01019 ANGIOTENSINOGEN PRECURSOR - Homo sapiens (Human), 485 aa.	3.90E-257	1 (1q42)
469	cg43918854	966	CTTCAACCCCTGGT CGGAGACAACGG A/C]TCACCATGGC CATCAGAACAGTG CG	A	C	Ile	Leu (698)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.30E-228	22 (22q11.2)
470	cg43918484	1148	CTGATTCTTCCGT TCTTCTTGACTTC /G]TGCCACCTTGC CAGCCAGCTGCT CG	C	G	Glu	Gln (699)	CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P05089 ARGINASE 1 (EC 3.5.3.1) (LIVER-TYPE ARGINASE) - Homo sapiens (Human), 322 aa.	1.30E-171	6 (6q23)

471	cg43942977	1009	ACGGCCCTGGAG AACCAGAAGAAG G[C/T]GAGGAAGA AGAAAGTCTTGAT TGCC	C	T	Ala	Val (700)	CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	
472	cg43942977	725	GGATGGTGTCTG ATGAGGAGTTGG A[G/T]CAGATGCT GGACAGTGGGCA AAGCG	G	T	Glu	Asp (701)	CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.60E-148	
473	cg43943361	921	TTGGGGTTGGCTT GGTTTCAATAAGI G/C]AACGGGGAC ACTTACAAATTGC TGC	G	C	Glu	Gln (702)	CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:P04179 SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) - Homo sapiens (Human), 222 aa.	5.70E-124 6 (6q25.3)	
474	cg25236776	1094	GTGACCCGAGCCC GAGTGCCCGCGAG G[G/T]CTTTCACC GCCGCGCCCGCG CCAGC	G	T	Gly	Val (703)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	

475	cg25236776	881	CAGTGCCTCCCT GCGGCCCGGG [G/T]CAAAGGCCG CTGCTTCGGGCC CAGC	G	T	Gly	Val (704)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.20E-91	
476	cg38899722	30	GGCCAACCTCTGCT ATGGACACACAG G/C]TACTCTGCTG TGGGTCATCTGT CT	G	C	Val	Leu (705)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G292791 T- CELL RECEPTOR BETA PRECURSOR - HOMO SAPIENS (HUMAN), 145 aa (fragment).	5.70E-75	
477	cg11753818	253	GCCTGGAACACC AGGCTCCTCTGC C[G/A]TGTCTGCT TTGTCTCCTGGGA GCA	G	A	Arg	His (706)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G2104755 T CELL RECEPTOR V-BETA 23 - HOMO SAPIENS (HUMAN), 129 aa (fragment).	1.30E-66	7
478	cg2526759	519	AGCCACCCAGAC CGGAGACTCGGC C[G/A]TCTACCTCT GTGCTGTGGAGG CCTA	G	A	Val	Ile (707)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	
479	cg2526759	539	CGGCCGTCTACC TCTGTGCTGTGGA [G/C]GCCTATTCTA ACGACTACAAGCT CA	G	C	Glu	Asp (708)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	

480	cg1902363	368	CAGAACAAAAGCA AATGGAATTGGA GTTAGCATCCTGG TGGCCCTGCTGC AGA	T	Glu	Asp (709)	CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P01286 SOMATOLIBERIN PRECURSOR (GROWTH HORMONE-RELEASING FACTOR) (GRF) (GROWTH HORMONE-RELEASING HORMONE) (GHRH) (SOMATOCRININ) - Homo sapiens (Human), 108 aa.	2.10E-52	
481	cg43277632	3110	GAAACCCGGAAG CACTGTAATTGCC [A/G]GGTCTATAAA TGCACATGGCTCT GT	G	Arg	Gly (710)	NON- CONSER VATIVE	ATPase_as sociated	Human Gene SWISSPROT- ID:P35670 COPPER- TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

482	cg43252813	2306	TGTATTCTGTAA TGCGCTGATGA C/TATATATGATG GTTATGGACCACC AC	C	T	Thr	Ile (711)	NON- CONSER VATIVE	ATPase_as sociated	Human Gene SWISSNEW- ID:Q04656 COPPER- TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.pcls:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE- ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0	X (Xq12)
483	cg43920913	929	GCCCCCTGAGCAG TCAGGACCCGGC TTC/TCCGTCCGT GAGTGCCACGAT CCCAG	C	T	Pro	Ser (712)	NON- CONSER VATIVE	biotindep	Human Gene SWISSPROT- ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
484	cg40310734	267	GGAGTGGGTGCT GCTGCTCTTGGG A/C/GCTTGTGCT GCCCTCCAGCC TGGGC	C	G	Pro	Ala (713)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIb) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)

485	cg40310734	3111	CGTGTCTCTCCCTC CCCTATGCCGGTG[C/G]CCCCGCTCA GCCTGCCCCCGAG GGGA	C	G	Pro	Ala (714)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17p (17q21.3 2)
486	cg43956560	777	GGGGTACTATGG GCCCCAGTGTCA G[T/C]TTGTGATTG AGTGTGAGCCTTT GGA	T	C	Phe	Leu (715)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)

487	cg43956560	837	GCTGGGTACCAT GGACTGTACTCAC IC/TTCITTTGGAAA CTTCAGCTTCAGC TC	C	T	Pro	Ser (716)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)
488	cg42388009	753	TGCAGAAAGGCAC CACAGAGACCGG A/A/GGCGAGGGC AAGGGCACCTCG AAGAC	A	G	Arg	Gly (717)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT- ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL- BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7.00E-172	4
489	cg43977436	1945	GTGTGTGTGTAAT GGTGTGGCTGTAI C/TJGCTCCAACCA AGATCTTATTACT GA	C	T	Arg	Cys (718)	NON- CONSER VATIVE	calcium_cha nnel	Human Gene SWISSPROT- ID:P21817 RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE CHANNEL) - HOMO SAPIENS (HUMAN), 5032 aa.	0	

490	cg43280376	1130	CGGAAGCTGGTG TCCTACTGCCCC [A/G]AAGTTGCA ACAACTGTTGCCC CTC	A	G	Gln	Arg (719)	NON- CONSER VATIVE	carboxylase	Human Gene SWISSPROT- ID:P38435 VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE (EC 6.4.-.-) (GAMMA-GLUTAMYL CARBOXYLASE) - HOMO SAPIENS (HUMAN), 758 aa.	0	2
491	cg42201364	1595	CCAGGGCCCTCCA GGTCCAAGAGGC C[A/C]CTCTGGAG AGCCTGGTCTTCC AGGG	A	C	Trp	Gly (720)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT- ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0	6
492	cg42201364	176	GTGTTTACGCTG AACGATACCAGG C/T]GCCCACAGG CATAAAAGGCCCA CTA	C	T	Thr	Met (721)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT- ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0	6
493	cg40339378	2855	TCCAGGAATACCA GGTCTGCCTGGT A/G]TTCCTGGAC AAGAGGATTAAAA GG	A	G	Ile	Thr (722)	NON- CONSER VATIVE	collagen	Human Gene SPTREMBL- ID:Q12823 A TYPE IV COLLAGEN - HOMO SAPIENS (HUMAN), 1690 aa (fragment).	0	X (Xq22)

494	cg43063256	606	AGACTGTGTTACC AACAGACCATGC[A/G]GAAGTCAAGT GCGATGTGAAGG CTT	A	G	Arg	Gly (723)	NON- CONSER VATIVE	complement	Human Gene SWISSNEW- ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.pcls:SWISSPROT-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0	1 (1p32)
495	cg44032748	414	CTCCAGTTCTACA ACTTGTGTAAGG[A/C]AAGCACAGTG TGGACAGGATTTC CA	A	C	Lys	Gln (724)	NON- CONSER VATIVE	complement	Human Gene SWISSPROT- ID:P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 584 aa.	0	1 (1p32)
496	cg43049885	533	CAGTTTGGGGGA CAGCCATGCACT G[A/C]GCCTCTGG TAGCCTTTCAACC ATGC	A	C	Glu	Ala (725)	NON- CONSER VATIVE	complement	Human Gene TREMBLNEW- ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0	5 (5p13)
497	cg21644442	1347	CCAGGCTCTCCC AGGATCTCATCAC [T/C]GCGCCCCCA GGGCCTCAGCAA CCCC	T	C	Leu	Pro (726)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT- ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)

498	cg2753430	279	CCAAGCTCCCATG ACCCAGACAACG] C/T]CCTTGAAGAC AAGCTGGGTTAAC TG	C	T	Pro	Ser (727)	NON- CONSER VATIVE	csf	Human Gene Similar to SWISSNEW- ID:P08700 INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY- STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF) - HOMO SAPIENS (HUMAN), 152 aa pcsl:SWISSPROT-ID:P08700 INTERLEUKIN-3 PRECURSOR (IL- 3) (MULTIPOTENTIAL COLONY- STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MAST-CELL GROWTH FACTOR) (MCGF) - HOMO SAPIENS (HUMAN), 152 aa.	1.10E-77	5
499	cg43923204	1651	TCCACGTAGAAGC GGAAGCCGAGGT] A/G]GGAGATGTAC GCATTGATGGAA GG	A	G	Tyr	His (728)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

500	cg44017721	174	TTGGTAGGGACG GAACTCGGGCG C[G/T]GGCGGTGG CCCGAGTGGAGA TAGGA	G	T	Pro	Gln (729)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa.	2.40E-52	22
501	cg41626024	279	GCTGGTTTGCTCC CAGGAGGCCAAG[A/C]AGTCAGCCTA CTGCCCCCTACAGT CA	A	C	Lys	Gln (730)	NON- CONSER VATIVE	deaminase	Human Gene Similar to SWISSPROT-ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa.[pcIs:TREMBLNEW-ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.80E-78	1 (1p36.2)
502	cg43057018	1618	AAGCATCCGAACA ATCCTCATCTTT[T/ G]GAAGATGCCAG GAGCAATTCCGAA T	T	G	End	Gly (731)	NON- CONSER VATIVE	dehydrogenase	Human Gene SWISSNEW- ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.[pcIs:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)

503	cg42837709	464	CCGCACCAACGC CGACATCATCGAG [A/G]CCCTGAGGA AGAAAGGGCTTCAA GGG	A	G	Thr	Ala (732)	NON- CONSER VATIVE	dna_rna_bi nd	Human Gene Similar to TREMBLNEW-ID:G913312 DNA BINDING PROTEIN MEF2 {CLONE XMEF2A1} - XENOPUS LAEVIS, 516 aa.	3.90E-86	1
504	cg43327954	2205	TCCACGACCGGG TAGAGAACTACAA [C/A]CCGCGGCAG CGCAAGCTCCGC AACC	C	A	Asn	Lys (733)	NON- CONSER VATIVE	dna_rna_bi nd	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.50E-57	1
505	cg43971258	707	TCGTTGGAGATGA CAAGTCCCGAG[C/T]GAGCTCGGCT GTCTGGATGGGA AGG	C	T	Ala	Thr (734)	NON- CONSER VATIVE	dna_rna_bi nd_inhib	Human Gene Similar to SWISSNEW- ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX- LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa. ipcls:SWISSPROT-ID:Q02535 DNA-BINDING PROTEIN INHIBITOR ID-3 (ID-LIKE PROTEIN INHIBITOR HLH 1R21) (HELIX-LOOP-HELIX PROTEIN HEIR-1) - HOMO SAPIENS (HUMAN), 119 aa.	1.30E-60 (1p36.13)	1

506	cg41554010	1253	AGCTGGAGCAAC AGCAGGAACAGC AIG/TTCAGGAGCA GCAGCAGGAGCA GGTGC	G	T	Gln	His (735)	NON- CONSER VATIVE	eph	Human Gene SWISSNEW- ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.lpcis:SWISSPROT-ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203	11 (11q23)
507	cg43957743	1063	GTTTGGCATACT GGATATTTTAATTC TTCAGTGGAGATA AAAGACAGCCCCA CT	C	T	Gly	Glu (736)	NON- CONSER VATIVE	esterase	Human Gene SWISSNEW- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).lpcis:SWISSPROT- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.90E-178	

508	cg43957743	1079	TATTTTAATCCAG TGGAGATAAAAGI A/C]CAGCCCACTA GGAAGTATATCAA TA	A	C	Ser	Ala (737)	NON- CONSER VATIVE	esterase	Human Gene SWISSNEW- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). pcis:SWISSPROT- ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAKYLPHOSPHATASE 3) (A- ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.90E-178	
509	cg43248101	812	AAGTGAATTCTAT CTTGCAATGAAC[A/GJAGGAAGGAAA ACTCTATGCAAAG AA	A	G	Lys	Glu (738)	NON- CONSER VATIVE	fgf	Human Gene Homologous to SWISSPROT-ID:P21781 KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR- 7) (FGF-7) (HBGF-7) - HOMO SAPIENS (HUMAN), 194 aa.	9.30E-106	15 (15q15)

510	cg43969014	332	GATGAGCTCTCCA ACCACGTATTTTC /A/TGCGTTTTGA TCCAGACCCAGAT G	C	A	Arg	Ile (739)	NON- CONSER VATIVE	glucuronida se	Human Gene Similar to SWISSPROT-ID:P08236 BETA- GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.40E-80	5
511	cg43286488	387	CACCAGCAAGAT GCCACGATCAG C[G/C]GAACCTGC CCAAGGCCTGCTT CTTG	G	C	Pro	Arg (740)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSNEW- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE- SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.lpcis:SWISSPROT-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0	12

512	cg44004239	663	TTTTCCCAGGGG TCACAGACTGAT A/GJACCCACAGAG GTCAGGGTCTTCT GT	A	G	Tyr	His (741)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN- DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
513	cg44004239	672	GGGGTCACAGAC TGATAACCCACAG [A/G]GGTCAGGGT CTTCTGTCCAGTG GTC	A	G	Ser	Pro (742)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN- DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
514	cg44004239	773	CTGATGACCCACA GAAGTCATGGTC A/GJTTGCCCCAGT GATCTCAGTCTTC TC	A	G	Met	Thr (743)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT- ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN- DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	

515	cg43932434	1504	ATATGTGTCATAC TGGGAGGTGTTG] G/TATGTGAGGAT GTACACCCCTGTG TT	G	T	Ser	Tyr (744)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT- ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYtic GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.80E-195	11 (11pter)
516	cg40915005	622	AAGGAGCCTCTCT CCTTCCATGTCA] C/TCTGGATCGCA TCCTTTTACAACC AT	C	T	Thr	Ile (745)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSNEW- ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T- CELL SURFACE ANTIGEN T6/LEU- 6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa. pcds:SWISSPROT-ID:P06126 T- CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)

517	cg40915005	737	ATTCCAGCACCAT CGTTTTCCTGTG G/CJCCCTGGTCCA GGGAAACTTCA GCA	G	C	Trp	Cys (746)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSNEW- ID:P06126 T-CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T- CELL SURFACE ANTIGEN T6/LEU- 6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa. pcds: SWISSPROT-ID: P06126 T- CELL SURFACE GLYCOPROTEIN CD1A PRECURSOR (CD1A ANTIGEN) (T-CELL SURFACE ANTIGEN T6/LEU-6) (HTA1 THYMOCYTE ANTIGEN) - HOMO SAPIENS (HUMAN), 327 aa.	2.00E-183	1 (1q21)
518	cg36834323	1529	GTGCTCCCTGATC CTCGTGAAGCAT A/GJTGCTAGCTCA AGTTATGTGGCAT CT	A	G	Tyr	Cys (747)	NON- CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID: P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
519	cg36834323	329	AATGCTGCGAAAG ATATGAATGGAAJA /CJGTCTTTGCATG GAAAAGCAATAA A	A	C	Lys	Thr (748)	NON- CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID: P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	

520	cg36834323	463	AAGTCTGAGATCT GCAAGAGGAAGC[A/C]GTGGAGGAA CAAGAGGGTGGC TTCC	A	C	Ser	Arg (749)	NON- CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
521	cg44019290	1697	GCGGATAAGTAG AGGACCTTCATGT [T/G]GTATTTCGTG GTGAAGTTGGTTC GG	T	G	Asn	His (750)	NON- CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.50E-80	11
522	cg42336656	1665	CTTAGACATACAA TATACCTTACCTTA/ GJGAGGTCACGTA TGTTTGTCGCCAC A	A	G	Arg	Gly (751)	NON- CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q05910 CELL SURFACE ANTIGEN MS2 PRECURSOR (EC 3.4.24.-) (MACROPHAGE CYSTEINE- RICH GLYCOPROTEIN) (CD156 ANTIGEN) - MUS MUSCULUS (MOUSE), 826 aa.	9.40E-58	
523	cg42730678	980	GGAGCGAGCGTG GATCCAGTTCGC GIGTJCGGGGTG TTTGGGTCAAGTT GCTG	G	T	Ala	Asp (752)	NON- CONSER VATIVE	homeobox	Human Gene SWISSPROT- ID:P28356 HOMEBOX PROTEIN HOX-D9 (HOX-4C) (HOX-5.2) - HOMO SAPIENS (HUMAN), 342 aa.	2.60E-188	2

524	cg42714160	769	GCCCTGTGCCCTG ACGGAGAGGCAG ATTGJCAAGATATG GTTCCAGAACCGA CGC	T	G	Ile	Ser (753)	NON- CONSER VATIVE	homeobox	Human Gene Homologous to SWISSPROT-ID:P17509 HOMEBOX PROTEIN HOX-B6 (HOX-2B) (HOX-2.2) (HU-2) - HOMO SAPIENS (HUMAN), 224 aa.	1.10E-123	
525	cg42359655	3297	CTGGGCACCATAT AGGATAGCCCCAC A/GJCCGTCATCAA AGCCCATGCCAG AGT	A	G	Thr	Ala (754)	NON- CONSER VATIVE	hydrolase	Human Gene SWISSPROT- ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYL CERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)
526	cg43925670	2172	GTGGAGGGTGCA GGTGAAGTAGCAT IC/GJCACTTCCTTC TTCCTCTTTCTTG AT	C	G	Asp	His (755)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.pcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1

527	cg43090990	1083	TGCTCCATCAAAA ATGAAGCAAGGC[C/T]GCCATGTTTA CCGACACCGGGA AAA	C	T	Pro	Leu (756)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:Q04759 PROTEIN KINASE C, THETA TYPE (EC 2.7.1.-) (NPKC- THETA) - HOMO SAPIENS (HUMAN), 706 aa.	0	10
528	cg43969763	2663	CAAAAGCAAGAAA GTTCTTTGAGAA[G/T]TTGCCAGATG GCAC TTGGAAC TT AA	G	T	Lys	Asn (757)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:Q13627 SERINE/THREONINE- SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK) - HOMO SAPIENS (HUMAN), 763 aa.	0	21 (21q22.1)
529	cg43932396	1226	AGTCCACCGCCG CCTCAGGCCCGTG C[C/T]GCTGGCCG AGTAGGAGAACT GGGG	C	T	Gly	Ser (758)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:P31749 RAC-ALPHA SERINE/THREONINE KINASE (EC 2.7.1.-) (RAC-PK-ALPHA) (PROTEIN KINASE B) (PKB) (C-AKT) - HOMO SAPIENS (HUMAN), 480 aa.	1.40E-262	14 (14q32.3)
530	cg43917871	1429	GGCACTGAAGAA ATCCCTGACATCA [T/C]ATTGGCGCT GCTGACGGGCGT ACTG	T	C	Met	Val (759)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
531	cg43917871	1621	GGGCTGACAAGG TGCTGATTTTCAC[T/G]GTGGACAAAG CGTTCCCATCGCT TT	T	G	Ser	Arg (760)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)

532	cg43917871	1713	T	TCAATGTTGTAT TTGTCAATATAGT /C/CATATAAATCTT CTGTCCCCAGAAC	C	Asp	Gly (761)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
533	cg43917871	2096	T	TGTAAATCGAAT ATCATAGTCTGT /G/AACGTCCTGGTA CAATTGCTTGAAG T	G	Leu	Phe (762)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT- ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
534	cg43322545	1107	A	TCGGCTAGGCAG CCTCCATCCTCAG [A/C]CCCCCTTATCA CATCCGCGGTGGC ATG	C	Thr	Pro (763)	NON- CONSER VATIVE	kinaserecep tor	Human Gene SWISSNEW- ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. pcls:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)

535	cg43322545	2116	TTCCTCCTCTATT CCCGGCTCGGGG [A/G]CCAGCCAGT GTACCTGCCCACT CAG	A	G	Asp	Gly (764)	NON- CONSER VATIVE	kinaserecep tor	Human Gene SWISSNEW- ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcds:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
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536	cg43958558	863	TCCGGGATAAGCT CCAGGTGCTCCAI G/TGGTAGCGC CTGGAGGTGCCT GTCC	G	T	Pro	His (765)	NON- CONSER VATIVE	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN- 3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ- BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE- SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.90E-139	14 (14q21)
537	cg43966144	718	AAGCTTGTCATGC CTCACAGCAGTGI C/AJGCACAAGACT GCCCAGCCCCAAT GGA	C	A	Ala	Glu (766)	NON- CONSER VATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147	6 (6p21.3)

538	cg43966144	823	ACTTACACCTGTG TGGTAGAGCACAT T/CJTGGGGCTCCT GAGCCCATCCTTC GG	T	C	Ile	Thr (767)	NON- CONSER VATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.10E-147	6 (6p21.3)
539	cg42686658	907	GGCCTGGTGGGC TTCCCTCGTGGGCA [C/T]CGTCCTCATC ATCATGGGCACAT AT	C	T	Thr	Ile (768)	NON- CONSER VATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
540	cg38337333	1044	CTGAGCCCCAGAG CGTTGTCTCCTGC [C/G]CATGAGCAC CACAGTCAGGCC TTGA	C	G	Pro	Ala (769)	NON- CONSER VATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
541	cg38337333	424	AGCCCGGCCGGG CCCCACGGTTCCG C[A/G]CAGGAGAG AACGTGACCTTGT CCTG	A	G	Thr	Ala (770)	NON- CONSER VATIVE	MHC	Human Gene Homologous to SPTREMBL-ID:Q95368 HLA CLASS I INHIBITORY NK RECEPTOR - HOMO SAPIENS (HUMAN), 455 aa.	1.80E-113	19
542	cg42481172	340	CCGGCTGTGCTC AGGGGTGTGGGG TIA/GJCGGATACA GAGGAGCGGCTG GTGGA	A	G	Thr	Ala (771)	NON- CONSER VATIVE	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.30E-71	1

543	cg3000465	238	GAAGATGCCCTC CTCAGACATGAGT [G/T]GAAAGGTTAT CAGAAATGGGTC CGC	G	T	Trp	Leu (772)	NON- CONSER VATIVE	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	6.10E-70	8 (8p11.2)
544	cg3000465	240	AGATGCCCTCCTC AGACATGAGTGG[A/C]AAGGTTATCA GAAATGGGTCCG CCC	A	C	Lys	Gln (773)	NON- CONSER VATIVE	misc_chann el	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	6.10E-70	8 (8p11.2)
545	cg43249083	1067	GCCTCGGGCTTC CACTACGGTGTG C[A/T]CGCCTGCG AGGGCTGCAAGG GCTTT	A	T	His	Leu (774)	NON- CONSER VATIVE	nucl_recpt	Human Gene SWISSPROT- ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
546	cg44928796	68	AGCGGACGGTC CGGAGCAAGCCC A[G/C]AGGCAGAG GAGCGACAGAG GGAAA	G	C	Gln	His (775)	NON- CONSER VATIVE	nucl_recpt	Human Gene SWISSNEW- ID:P10275 ANDROGEN RECEPTOR - HOMO SAPIENS (HUMAN), 919 aa. lpcds:SWISSPROT-ID:P10275 ANDROGEN RECEPTOR - HOMO SAPIENS (HUMAN), 919 aa.	0	X
547	cg43323772	91	GTCCCGGGAGTG AGCGATGAGCTG G[C/T]TCTGTTC TGGCCACACAGAG TCGC	C	T	Leu	Phe (776)	NON- CONSER VATIVE	nuclease	Human Gene TREMBLNEW- ID:G2935442 RIBONUCLEASE H1 - HOMO SAPIENS (HUMAN), 286 aa. lpcds:TREMBLNEW-ID:G2935444 RIBONUCLEASE H1 - HOMO SAPIENS (HUMAN), 286 aa.	1.40E-157	

548	cg42732993	809	GGCTATAATCACA ATGGGAATGGT G/TJGAAGCCCAA ACCAAAAATGGCC AA	G	T	Cys	Phe (777)	NON- CONSER VATIVE	oncogene	Human Gene Homologous to SP TREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN - HOMO SAPIENS (HUMAN), 284 aa (fragment).	6.00E-150	
549	cg42904626	155	ATATAAACTTGTG GTAGTTGGAGCT G/TJGTGCCGTAG GCAAGAGTGCCTT GAC	G	T	Gly	Cys (778)	NON- CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:P01118 TRANSFORMING PROTEIN P21/K- RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
550	cg42904626	304	TGGATATTCTCGA CACAGCAGGTCA A/CJGAGGAGTACA GTGCAATGAGGG ACC	A	C	Gln	His (779)	NON- CONSER VATIVE	oncogene	Human Gene Similar to SWISSPROT-ID:P01118 TRANSFORMING PROTEIN P21/K- RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.10E-97	12
551	cg42691989	706	CTGTTCCAGGATCT CCTCATTTCTGAC A/TJGTTCCTCTGAT GTCCAAAATTGGTT G	A	T	Cys	Ser (780)	NON- CONSER VATIVE	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE- GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE-RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.90E-101	14 (1)

552	cg43917453	4096	AGGTCCCTCGCGG AGCTGGGTCCGG G/A/G]CCCGGGAG GGTAGGTCAGCG CAGAC	A	G	Ser	Pro (781)	NON- CONSER VATIVE	phosphatas e	Human Gene TREMBLNEW- ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0	7
553	cg43947363	368	CTGGCGCACTACT CGGACCTGCTCC[C/T]CCTGGCGGG CCTGGGGCTGAT TGAG	C	T	Gly	Glu (782)	NON- CONSER VATIVE	phosphatas e	Human Gene SWISSPROT- ID:P23469 PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON) - HOMO SAPIENS (HUMAN), 700 aa.	0	
554	cg43928335	3187	GCACAAGGAACG GAATTGCTGTCTG [A/G]TTTCTGCTTT AACAGCATTTGAT GC	A	G	Ile	Thr (783)	NON- CONSER VATIVE	phosphatas e	Human Gene SWISSPROT- ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.20E-302	11 (11q22)
555	cg43996195	1330	CTTCGGGGAAAG TTGGGGATTTCAC [C/T]GTAGTCAAAG ATCTGGGCCCTGA GTT	C	T	Gly	Ser (784)	NON- CONSER VATIVE	phosphoryla se	Human Gene SWISSPROT- ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.40E-155	

556	cg44022214	3340	AGGTCCTCCTCGA ATTGGGATGGCC A/GAGGTGCATCA TCATCATCCCAGA GG	A	G	Trp	Arg (785)	NON- CONSER VATIVE	polymerase	Human Gene SWISSNEW- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa pcids:SWISSPROT-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
557	cg43958858	1593	CTCAGACCATGTC CTTCGGATGCACI C/G GTTACAGAGC ACCTGGGGAGCA GGA	C	G	Arg	Gly (786)	NON- CONSER VATIVE	polymerase	Human Gene SWISSNEW- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa pcids:SWISSPROT-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)

558	cg42534568	641	CGCTTTGAGACG CAGCTGGGCACC C/ATJGGCGCAGT TCCCAACACACT CCTG	A	T	Gln	Leu (787)	NON- CONSER VATIVE	potassium_ channel	Human Gene SWISSPROT- ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
559	cg42534568	868	GGGGACGAGGC CATGGAGCGC.TT C/C/GJGCGAGGAT GAGGGCTTCATTA AAGA	C	G	Arg	Gly (788)	NON- CONSER VATIVE	potassium_ channel	Human Gene SWISSPROT- ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
560	cg42534568	910	CATTAAAGAAAGAG GAGAAAGCCCCTG C/GJCCCCGCAACG AGTCCAGCGCC AGGT	C	G	Pro	Ala (789)	NON- CONSER VATIVE	potassium_ channel	Human Gene SWISSPROT- ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
561	cg43154190	898	TGGAGGGGATGC TCATTTTGATGAA G/CJATGAAAGGTG GACCAACAATTTC AG	G	C	Asp	His (790)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSPROT-ID:P50280 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE- 7) (MMP-7) (MATRIN) - RATTUS NORVEGICUS (RAT), 267 aa.	2.40E-59	11 (11p13)

562	cg43154190	923	GATGAAAGGTGG ACCAACAATTTCAG G/CJAGAGTACAAC TTACATCGTGTG CG	G	C	Arg	Thr (791)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSPROT-ID:P50280 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE- 7) (MMP-7) (MATRIN) - RATTUS NORVEGICUS (RAT), 267 aa.	2.40E-59	11 (11q22)
563	cg43927549	694	ATTCTACGATTCC GGTTTGCTCCAGI G/TJGTAACTAGC GCTCCTTTCCGTA AC	G	T	Gly	Cys (792)	NON- CONSER VATIVE	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
564	cg43325541	1081	CGCTGCCCTTCTCC CGAAAGGTCTGCI C/TJCCCTTCACGCG TTCGGCTTCCCGC AG	C	T	Gly	Glu (793)	NON- CONSER VATIVE	synthase	Human Gene TREMBLNEW- ID:G2725625 ACETOLACTATE SYNTHASE - HOMO SAPIENS (HUMAN), 632 aa.	0	19

565	cg43064068	1474	GTGAAGGCATTG TGGTCCTGGCCTI C/TJGCAGTTCCTG TCCCATGACCCAG AA	C	T	Ser	Leu (794)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
566	cg43064068	1617	GACTGTCAACAGG GAAAATTCAACGA [G/A]CCAAGCTTC GAGACAAAGGAGT GGAA	G	A	Ala	Thr (795)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.jpcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL- COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	

567	cg36988276	1119	GCAAGAAGTTGAT TATATGACTCAGIA /GICTAGGGGTCA GAGATCCCTCTG GC	A	G	Thr	Ala (796)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
568	cg36988276	535	AAGGCCAACAAAC CTGCTCTACATCA[A/C]CCCTGAGGC CTTCCAGAACCTT CCC	A	C	Asn	Thr (797)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
569	cg32296848	1475	GAATGTCTTGAGA ATCCAGTGCTCT[C/T]GCAGAAAGCA GTCTTCCAAACAT GC	C	T	Arg	Cys (798)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A-ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	1.60E-252	8 (8p21)
570	cg2524739	1590	TCTCTCTGGAGAA GATCCCAACCCAT[C/G]ACACAAAACG GTCAGCACCCCAA CCT	C	G	Ile	Met (799)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P21728 D(1A) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 446 aa.	8.30E-240	5 (5q35.1)

571	cg2320320	394	AGTGTCTGGATGA TCTTTGTGGTCA[C /T]TGCATCCGTTT TCACAAATGGGCT T	C	T	Thr	Ile (800)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT- ID:P04001 GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) - HOMO SAPIENS (HUMAN), 364 aa.	8.50E-199	
572	cg43264978	519	CATCTTCTCCATC AACCTCTTCAGC[A/G]GCATTTTCTT CCTCACGTGCATG AG	A	G	Ser	Gly (801)	NON- CONSER VATIVE	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
573	cg3003708	285	TCTTTTGTGGACA TCTGCTTCTCCTTT /C]CACACCCGTCC CCAAGATGCTGG CC	T	C	Phe	Ser (802)	NON- CONSER VATIVE	tm7	Human Gene TREMBLNEW- ID:E1246031 OLFACTORY RECEPTOR - HOMO SAPIENS (HUMAN), 312 aa.	2.50E-160	
574	cg38841806	68	GGCCCTGAGAGC AACACACACGGGC A/T]C]CACAGCCTT CTCCATGCCCCAG CTGG	T	C	Ile	Thr (803)	NON- CONSER VATIVE	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
575	cg43336100	688	TGGAAGCGTGCA TCCAGTGAGACCA [A/T]TGAGGCTTGA GTCITTTAGTGCC TG	A	T	Met	Leu (804)	NON- CONSER VATIVE	tnf	Human Gene SWISSPROT- ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)

576	cg43335562	234	GAGGCGCGGGGA GCCAGGCCTGGG C/T/C]CCGGGTCC CCAAGACCCCTTGT GCTC	T	C	Leu	Pro (805)	NON- CONSER VATIVE	tnfreceptor	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-55	8
577	cg43140548	2857	ACTCGCACGTGG ATCCTGAGGCTGT [A/G]AGAGGTAAG GAAGGCTTTGCCA CAG	A	G	Tyr	His (806)	NON- CONSER VATIVE	transcriptfac tor	Human Gene SPTREMBL- ID:Q14872 METAL-REGULATORY TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 753 aa.	0	1
578	cg43011561	1285	CATTGACAGCGA GGCCTCCTCAGC C/C/T]TCTTCATGG CGAAGAAGAAGA CGCC	C	T	Leu	Phe (807)	NON- CONSER VATIVE	transcriptfac tor	Human Gene SWISSPROT- ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TFIIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.30E-275	19 (19p13.3)
579	cg43998970	1346	TGACAGAGCTGTA CCGTGACATTTTTC /G]CAGCACCTTCG GGATGAATCAGG CA	C	G	Phe	Leu (808)	NON- CONSER VATIVE	transcriptfac tor	Human Gene SPTREMBL- ID:Q07279 TRANSCRIPTION FACTOR NF-E2 - MUS MUSCULUS (MOUSE), 373 aa.	1.70E-177	12

580	cg2537639	464	CACTACTATGTCT TCACCGACCCAGC[C/TGGCCCGCGGT GCCCCGCGTGAC GCTG	T	Pro	Leu (809)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYLTRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
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581	cg2537639	523	TCGGCAGCTGTC AGTGCTGGAGGT G[C/G]GCGCCTAC AAGCGCTGGCAG GACGT	G	Arg	Gly (810)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYL TRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9954)
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582	cg2537639	643	GGTGTGCGTGGA CGTGGACATGGA G[T/A]TCCGCGAC CACGTGGGCGTG GAGAT	T	A	Phe	Ile (811)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYL TRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
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583	cg2537639	700	TCCGCTGTTCCG CACCTGCACCC C[G/A]GCTTCTAC GGAAGCAGCCGG GAGGC	G	A	Gly	Ser (812)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYL TRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
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584	cg2537639	793	CAAGGACGAGGG CGATTCTACTAC C/ATGGGGGGGT TCTTCGGGGGGT CGGT	C	A	Leu	Met (813)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYLTRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
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585	cg2537639	826	GTTCTTCGGGGG GTCGGTGCAAGA G[G/A]TGCAGCGG CTCACCAGGGCC TGCCA	G	A	Val	Met (814)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT- ID:P16442 FUCOSYLGLYCOPROTEIN ALPHA- N- ACETYL GALACTOSAMINYLTRANS FERASE (EC 2.4.1.40) (HISTO- BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3- ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.50E-192	9 (9q34)
586	cg42742340	3249	CACATCGTGGTG GAGCTGACCCAG G[C/A]TGACGCTTT GGGCTCCAGGTG GCGG	C	A	Ala	Asp (815)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCYTE-SPECIFIC TRANSPORTER PROTEIN) - HOMO SAPIENS (HUMAN), 838 aa.	0	15
587	cg41653463	427	GTCTGAAAGATT CCACAAGGACAT C[G]CTGAAGCCCT CACCAGGGAAGA GCC	C	G	Ile	Met (816)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0	3 (3p25)

588	cg40351913	1165	CAAGTTCACCAAC AACTGCTACAGG G/CJACGCGATTGT CACCACCTCCATC AA	G	C	Asp	His (817)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
589	cg40351913	1232	TCCTCCGGCTTCG TCGTCTTCTCCTTT /CJCTGGGGTACA TGGCACAGAAGC AC	T	C	Phe	Ser (818)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT- ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
590	cg43955093	4776	CTGCGGTAGCTG TCCCAGGCGCTCG G/C/GJCCGCGCCG CCTCGTCCATGTT GAGG	C	G	Ala	Pro (819)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0	16
591	cg43055918	522	GCATAGGACATG GCGGGCTTGCCC C/C/GJCGCAGAGC TCTGGGGGCTAC TGCTA	C	G	Gly	Arg (820)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
592	cg43968854	4604	CAACCCCTAGAAG ACCTGGCTGGCTT T/GJGAAAGAGCTC TTCCAGACACCAG TA	T	G	Leu	Trp (821)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSNEW- ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)

593	cg43070241	1841	CCATTGTTCAAGA CATCCTACGTTT[T /G]GAAATGCCTGC AAGCAAAATTGTC C	T	G	Phe	Leu (822)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P55157 MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN, LARGE SUBUNIT PRECURSOR - Homo sapiens (Human), 894 aa.	0	4 (4q22)
594	cg43262121	2001	ACAAATTCAGAGAG GGAGACTGAGCA[G/T]ACACCAGCAT TGATCATGGTGCC AA	G	T	Gln	His (823)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
595	cg43262121	553	ATCAGGAAAAGGT GTTGGATCACTGG [A/T]GCATCATGAC CAGTGAGGAAGA AGT	A	T	Ser	Cys (824)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
596	cg43262121	937	CCCCAAACAGGA AGTCCATGGGCC C[A/T]ACCCCTGACA GCAGCTTCTTAAC TTC	A	T	Asn	Tyr (825)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	
597	cg43262121	938	CCCCAAACAGGAA GTCCATGGGCC A[A/T]CCCTGACA GCAGCTTCTTAAC TTCC	A	T	Asn	Ile (826)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SPTREMBL- ACC:Q15840 ZINC FINGER PROTEIN BASONUCLIN - HOMO SAPIENS (HUMAN), 994 aa.	0	

598	cg44024279	501	CTGGAAGAACTTT GCCATGAGAAAG] A/GJAATTTTGAG AAGTACGGACATT CA	A	G	Glu	Gly (827)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P02771 ALPHA- FETOPROTEIN PRECURSOR (ALPHA-FETOGLOBULIN) (ALPHA- 1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
599	cg44928804	1235	AATGATTAAACAAC AACCTGAGACACI G/AJCGGATGAAAT GTTCTGGAACCCAC GT	G	A	Ala	Thr (828)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
600	cg43317253	367	GCCCCCAGGCAT GGCTAGCTCGTG TIG/TJCCGTGCAG GTGAAGCTGGAG CTGGG	G	T	Ala	Ser (829)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSNEW- ACC:P42568 AF-9 PROTEIN - Homo sapiens (Human), 568 aa.	2.00E-301	9
601	cg41637661	223	CAGCTTTCATCC ATTTTATTATIG/ AJGACATACTGCT AGTGGAAGACCT A	G	A	Gly	Arg (830)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSNEW- ACC:O43913 ORIGIN RECOGNITION COMPLEX SUBUNIT 5 - Homo sapiens (Human), 435 aa.	6.10E-236	
602	cg42913861	3034	CAGGTGTCCTGC GAGCCACCCGGG GJACJTCCGGGTG GCGGGGGTGGCG GCGGC	A	C	Ser	Ala (831)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09529 INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) - Homo sapiens (Human), 407 aa.	3.00E-227	2 (2cen)

603	cg43249389	526	AGAGGAGAGAGC CGCCCTCGAGCG G[A/G]GCAAGGCG ATTGAGAAAAACC TCAA	A	G	Ser	Gly (832)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
604	cg43919239	335	GCCAGAGTTGCA GCATCAGGGCCA G[A/C]CTGAGCAG GAGACCCCCAGT CCCAT	A	C	Ser	Arg (833)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.20E-150	
605	cg41642952	787	TAGGAATGACAGC AGTAGCAGTAAT A/G[GGAAAGGCCA AAAATCCCCCTGG AGA	A	G	Arg	Gly (834)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P21583 STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND) - Homo sapiens (Human), 273 aa.	3.70E-142	12

606	cg43945147	221	TGTTCTGTGAGCC TCAATGGTACAG G/CJGTGCTCGAG AAGACAGTGTG ACTC	G	C	Arg	Ser (835)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:P08637 LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR III-1 PRECURSOR (FC- GAMMA RIII) (FCRIII) (IGG FC RECEPTOR III-1) (FC-GAMMA RIII-ALPHA) (CD16) (FCR-10) - Homo sapiens (Human), 254 aa.	1.60E-134	1
607	cg43926002	391	GGGCACAGAAAC ACAGCAGCGGA G/C/SJAGCAACAC CAGCACTGCCAA CAGAT	C	S	Ser	??? (836)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.60E-116	10
608	cg43972311	1609	ATTGCCATTGTGG TAACTCTGGGTCI T/GJCATCATCTTC AGTGCCCCCAATTG TG	T	G	Glu	Ala (837)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:AAD38008 GLYOXALASE-I (EC 4.4.1.5) - HOMO SAPIENS (HUMAN), 184 aa.	2.20E-98	6
609	cg42556108	521	GTGAAGCGGTGT ATGGGGACAGTG A/C/AJCCTCAACCA GGCCAGGGGCTC CTTT	C	A	Thr	Asn (838)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P49913 ANTIBACTERIAL PROTEIN FALL-39 PRECURSOR (FALL-39 PEPTIDE ANTIBIOTIC) (ANTIMICROBIAL PROTEIN CAP-18) (LL-37) - Homo sapiens (Human), 170 aa.	2.90E-87	3

610	cg36842490	487	AGTGACTTCAGTA AACTCTTGGTCT A/CJACTTTCTGCC AAAAAGTACCTTG AG	A	C	Gln	Pro (839)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSPROT-ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa.	2.30E-85	
611	cg43942549	1052	CGGTATAACGTCA AAAATCCTGTTT[G /TTTCAGCCCAAGGT TCAGAAATTGCCT C	G	T	Val	Phe (840)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:Q94218 CODED FOR BY C. ELEGANS CDNA CM10H5 - CAENORHABDITIS ELEGANS, 589 aa.	2.80E-73	4
612	cg42381630	283	AAGGCGCTATGTA CAGCCTCCTGAA[A/GJTGATTGGGCC TATGCGGCCCGA GCA	A	G	Met	Val (841)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
613	cg42381630	505	TGAAGATGGTCCT GATGGGCAGGAG[A/GJTGACCCGC CAAATCCAGAGGA GGT	A	G	Met	Val (842)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
614	cg3004395	260	ATTACTGAAGGGT GGAGAACAGAAAG[G/CJGTCATGAAAA AATATCTGCTTCA TT	G	C	Gly	Arg (843)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G238693 T CELL RECEPTOR VARIABLE ALPHA CHAIN - HOMO SAPIENS (HUMAN), 143 aa (fragment).	1.00E-59	14 (14q11.2)

615	cg43960645	733	CACTTCCTCTTTC TCTTTGGATGCC ATTACCCCTCCTG TTGGGGGGCAGA TGG	A	T	Val	Glu (844)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to SWISSNEW- ACC:O76070 GAMMA-SYNUCLEIN (PERSYN) (BREAST CANCER- SPECIFIC GENE 1 PROTEIN) - Homo sapiens (Human), 127 aa.	1.20E-58	
616	cg2526759	289	GAAGACAAGGTG GTACAAAGCCCTC TTATCTCTCTGGTT GTCCACGAGGGA GAC	T	A	Leu	Gln (845)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	
617	cg2526759	342	TGTAACCTCTCAAT TGCAGTTATGAA GATGTGACTAATT TCGAAGCCTACTA TG	G	A	Val	Met (846)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	
618	cg2526759	364	GAAGTGACTAACT TTCGAAGCCTAC TATGTGTACAAG CAGGAAAAGAAA GCT	T	A	Leu	Gln (847)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	
619	cg2526759	475	AGCATATTAGATA AGAAAAGAACTTTT TCAGCATCCTGA ACATCACAGCCAC C	T	C	Phe	Ser (848)	NON- CONSER VATIVE	UNCLASSI FIED	Human Gene Similar to REMTREMBL-ACC:G33509 T CELL RECEPTOR - HOMO SAPIENS (HUMAN), 118 aa (fragment).	1.60E-54	

620	cg40310734	1067	TACAGAAATATGTC GTCGGTGCCCCC[gap/C]ACTTGGAG CTGGACCCTGGG AGCGG	gap	C	Thr	His (849)	FRAMES HIFT	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
621	cg40310734	3285	GTCGGCTTCTTCA AGCGGAACCGGC[gap/A]CACCCCTG GAAGAAGATGATG AAGA	gap	A	Pro	His (850)	FRAMES HIFT	cadherin	Human Gene SWISSPROT- ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
622	cg43956660	2521	GTCCATCACCTTCA CTTCAGTTATTCT[gap]CCTAGGAGGT TGTATAGTCTTCT GA	T	gap	Arg	Glu (851)	FRAMES HIFT	cadherin	Human Gene SWISSNEW- ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.lpcis:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.	1.80E-157	

623	cg43970982	2429	CTCCAGGGATAGT TGGACAGAAAGGG[gap/GJAGACCCTG GCTACCCAGGAC CAGCT	gap	G	Gly	Gly (852)	FRAMES HIFT	collagen	Human Gene SWISSPROT- ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
624	cg42175288	1837	GCTATGGAGGCA AAATGGGAGGAA G[gap/GJAAACGAC TACAGAAATGATC AGCGC	gap	G	Arg	Arg (853)	FRAMES HIFT	dna_rna_bi nd	Human Gene SPTREMBL- ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17
625	cg42175288	263	CGGTTACTCCAGT TATGGACAAAGT[ap/CJTATTCACAGT CCTATGGTGGTTA TG	gap	C	Tyr	Leu (854)	FRAMES HIFT	dna_rna_bi nd	Human Gene SPTREMBL- ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17
626	cg41554010	584	GGCCGAGCAGCT GCGGCGCCAGCT G[gap/GJACCCCT ACGCACAGCGCA TGGAGA	gap	G	Thr	Asp (855)	FRAMES HIFT	eph	Human Gene SWISSNEW- ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.lpcis:SWISSPROT-ID:P06727 APOLOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.80E-203	11 (11)
627	cg43065549	1553	CAGACTTCCACAG AGTGCTGGATGA[gap/AJCGCGGCCT GCCTTGCCCCCAG GGTTA	gap	A	Thr	Asn (856)	FRAMES HIFT	glycoprotein	Human Gene SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

628	cg41568631	999	TGACCACGGGGT GCTGGATGCCTG C[gap]/CJTATACAT CCTGGACCGCG GGGA	gap	C	Leu	Leu (857)	FRAMES HIFT	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
629	cg41637704	1220	GCGCCGCGAGAC AAGGCAGCGGA C[gap]/GJCGCCTGC GGACTTGAGGGA CAGTGA	gap	G	Pro	Arg (858)	FRAMES HIFT	homeobox	Human Gene SWISSPROT- ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.20E-224	7
630	cg43933380	364	ATAAGTTACAATG CTTTTTTTGTTT[A] gap]AAAAAAAAAA AAAGTCTGTACTT TA	A	gap	Leu	End (859)	FRAMES HIFT	interferon	Human Gene SWISSPROT- ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.40E-261	6
631	cg43072541	379	CTGTGGGGCTGG TTCTGTATCTGAT[gap/CJATCATTCTGA TTACGAAATAAAA CGT	gap	C	Ile	His (860)	FRAMES HIFT	kinase	Human Gene SPTREMBL- ID:Q15802 SERINE/THREONINE PROTEIN KINASE KRS-2 - HOMO SAPIENS (HUMAN), 487 aa.	9.60E-262	20

632	cg44032168	1536	GTCAGCCGCTAC CTCGACTGGATCC Ggap/TJATGGGCAC ATCAGAGACAAG GAAGC	gap	T	His	Leu (861)	FRAMES HIFT	protease	Human Gene Similar to SWISSPROT-ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.40E-82	2 (2q13)
633	cg43931248	1317	CCGGGCAGAGCT GCGTCTGCTGAG Ggap/GJCTCAAGT TAAAAGTGGAGCA GCACG	gap	G	Leu	Ala (862)	FRAMES HIFT	tgf	Human Gene SWISSPROT- ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.70E-214	19
634	cg43931248	1317	CCGGGCAGAGCT GCGTCTGCTGAG Ggap/GJCTCAAGT TAAAAGTGGAGCA GCACG	gap	G	Leu	Ala (863)	FRAMES HIFT	tgf	Human Gene SWISSPROT- ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.70E-214	19
635	cg43272560	847	AATCTCCGCACTG CAGGCCAGGGC Ggap/CJTGCCAGC TACAGAGAGAGG TCACA	gap	C	Ala	Ala (864)	FRAMES HIFT	tgfreceptor	Human Gene SWISSPROT- ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)

636	cg43266471	1067	CCAGGATCCATTT TGAGGATTATGGI gap/TJGTGCTGGG ACACCATCAACTC CTCA	gap	T	Gly	Gly (865)	FRAMES HIFT	tm7	Human Gene SWISSPROT- ID:P32241 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R- 1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP-R-2) - HOMO SAPIENS (HUMAN), 457 aa.	5.20E-254	3
637	cg43995237	625	CAAATCCCCCGT TTC TTCATCTTG[g ap/GJACATGCTAA AATGAAATTACGC AGT	gap	G	Gln	Pro (866)	FRAMES HIFT	transferase	Human Gene SWISSPROT- ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERAS E BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1

638	cg43995237	638	TTCTTCATCTTGA CATGCTAAATGlg ap/GjAAATTACGC AGTTTCTCTCTAT CAA	gap	G	Leu	Phe (867)	FRAMES HIFT	transferase	Human Gene SWISSPROT- ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERAS E BETA SUBUNIT) (RAB GERANYL- GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
639	cg43254094	267	CCGCCCTCTGCTG CTGCTGCTGCTG Cgap/GJGCGTCCC GCCAGCCGCAG CTTCCC	gap	G	Arg	Arg (868)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P78539 SUSHI REPEAT- CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.40E-257	X
640	cg44034555	665	ATCCAGGCTGAG CTGGATCATCTGA [G/gap]GGCCTCCA GCCACCCGTTTTC CCTT	G	gap	Pro	Leu (869)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.80E-252	1
641	cg44034555	667	CCAGGCTGAGCT GGATCATCTGAG G[gap]CCTCCAG CCACCCGTTTTC CTTGA	G	gap	Gly	Gly (870)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSNEW- ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.80E-252	1

642	cg39711096	882	AGCGAGTCCTCC GGGAGGCCACCA G[gap/G]TTACTGC CTCCAGCTGCAG CAGTGA	gap	G	Val	Gly (871)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
643	cg44128902	379	CGTTCAGAGGA GCATATCTGCTGA [gap/C]TGATGACC TGCAAGAGTCATC CAGA	gap	C	Asp	Asp (872)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201 (1p36.2)	
644	cg43946951	306	GGAACTCGAGCA CGTCGTCGGGG A[C/gap]CCCAAGA TCACCGGCGCCC TCTGGT	C	gap	Gly	Gly (873)	FRAMES HIFT	UNCLASSI FIED	Human Gene SWISSPROT- ACC:P09467 FRUCTOSE-1,6- BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6- BISPHOSPHATE 1- PHOSPHOHYDROLASE) (FBPASE) - Homo sapiens (Human), 337 aa.	3.50E-178 (9q22.2)	
645	cg43948890	195	ATCCCCGGGGGA GGGGCCCTGTA A[G/gap]GGAAACC AGACAAATCCCATG AGACT	G	gap	Pro	Leu (874)	FRAMES HIFT	UNCLASSI FIED	Human Gene Homologous to SPTREMBL-ACC:Q15182 SNRNP POLYPEPTIDE B - HOMO SAPIENS (HUMAN), 285 aa.	3.20E-147 20	
646	cg43948890	197	TCCCCGGGGGAGG GGGCCCTGTAAG G[G/gap]AAACCCAG ACAATCCCATGAG ACTCC	G	gap	Phe	Phe (875)	FRAMES HIFT	UNCLASSI FIED	Human Gene Homologous to SPTREMBL-ACC:Q15182 SNRNP POLYPEPTIDE B - HOMO SAPIENS (HUMAN), 285 aa.	3.20E-147 20	

647	cg43917524	713	GGGCCTGTCTGC CCAGTGGAGGAG G[C/gap]TTCCGCT GGTGTCTAGGG GGCATC	C	gap	Ala	Pro (876)	FRAMES HIFT	UNCLASSI FIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43025 PTD017 - HOMO SAPIENS (HUMAN), 258 aa.	3.20E-143	
648	cg43942004	373	CTCTCGGCACTG GTGACTGGCGAG A[gap]G[CCTGGAG CGGCTTCGGAGA GGGCTA	gap	G	Asp	Glu (877)	FRAMES HIFT	UNCLASSI FIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN-BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1.00E-107	5 (5q23)
649	cg43932428	681	TCGTGGCCAGGT CCTTCTGCGTAAG [C/gap]CCCTTGCT CTGCCGACCCTG CTGGA	C	gap	Gly	Gly (878)	FRAMES HIFT	UNCLASSI FIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.50E-72	
650	cg44010855	450	GGTCCAAATGCAA GTGCTCCCGGAA[G/gap]GGACCCAA GATCCGCTACAG CGACG	G	gap	Gly	Asp (879)	FRAMES HIFT	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5
651	cg44010855	452	TCCAAATGCAAGT GCTCCCGGAAGG[G/gap]ACCCCAAGA TCCGCTACAGCG ACGTG	G	gap	Gly	Asp (880)	FRAMES HIFT	UNCLASSI FIED	Human Gene Similar to TREMBLNEW-ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5